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APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 60/092,155
SARLIER APPLICATION NUMBER: 00/092,155
SARLIER APPLICATION NUMBER: 00/092,155
SOFTWARE: PatentIn Ver. 2.0
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US-08-832-874-49

US-08-832-874-49

US-08-884-324-13

US-09-117-914-6

US-09-817-180-3

US-09-817-180-3

US-09-818-17-13

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LOCATION: (35)

OTHER INFORMATION: N

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US-09-133-333-3

US-08-301-581-1

US-08-301-581-1

US-09-033-333-2

US-09-031-145-15

US-09-128-155-17

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ORGANISM: Homo sapiens
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GENERAL INCRMATION:
APPLICANT: Papsidero, Lawrence D
APPLICANT: Dapsidero, Lawrence D
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
BARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.0
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Patent No. 6306653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09146580A
Fatent No. 6306653
GENERAL INFORMATION:
APPLICANT: Paster, Lyn M
APPLICANT: Paster, Lyn M
APPLICANT: Prestact, Jana M
TILE REFERENCE: 200755/1002
CURRENT FILING DATE: 1998-09-103
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09146580A
Patent No. 6306653
GREAT INFORMATION:
APPLICANT: Papsidero, Lawrence D
APPLICANT: Syster, Lyn M
APPLICANT: Frustaci, Jan M
TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 202; DB 4; Length 311;
Pred. No. 1.4e-77;
0; Mismatches 2; Indels
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COTHER INFORMATION: N at position 162 is US-09-146-580-11
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Best Local Similarity 99.3%;
Matches 302; Conservative (
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Gaps
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                                                                                                                                                                                         3899 TITITITITIGAGACAGAGTCTCACTCTGTTGCCCAGGCTGGAGTGCAGTGGC 3950
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                                                                                     2.6%; Score 52; DB 4; Length 5835; 100.0%; Pred. No. 2.3e-13; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.3e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Calydon, Inc.
TITLE OF INVENTION: Prostrate
TITLE OF INVENTION: Prostrate
NUMBER OF SEQUENCES:
CORRESPONDENCES: ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcardero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTAM I.
REGISTRATION NUMBER: 20015
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/380,916
FILING DATE: 12-JAN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08380916
Patent No. 5648478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08721690; Patent No. 6057299; GENERAL INFORMATION: APPLICANT: Henderson, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-380-916-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                             52; Conservative
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Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                          Best Local Similarity
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            , us-09-033-33-3
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US-08-380-916-1
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US-08-721-690-1
                                                                                       Query Match
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APPLICANT: Yu, De Chao
APPLICANT: Schuur, Elic
APPLICANT: Schuur, Elic
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
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b; Pred. No. 1.5e-35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                               Query Match 5.2%; Score 104; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 104; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: WORKISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLIANG DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION UNDRER: 40,130
REFERENCE/DOCKET NUMBER: 3480'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TRIFFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09033333 Patent No. 6197293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERA: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5835 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-146-580-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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USA
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                                                                                                                                                                                     SEQ ID NO 8
LENGTH: 104
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                                                                                                                                                                                                                                 TYPE: DNA
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APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: MORISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 52; Conservative 0; Mismatches
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                  PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 30-7AN-1995
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENDE/DOCKET NUMBER: 34802-20001
TELECOMUNICATION INFORMATION:
TELECHOME: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/09033333; Patent No. 6197293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 3480
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                     TELEFAX: 415-494-0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: S815 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-891-581-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-033-333-2
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APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: TISSUE SPECIFIC ENHANCER ACTIVE
TITLE OF INVENTION: IN PROSTATE
  TISSUE-SPECIFIC ENHANCER ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%; Score 52; DB 3; Lei
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                   COMPUTER: USA
ZIP: 94304-1018
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,690
FILING DATE: 37-SEP-1996
FILING DATE: 37-SEP-1996
FILING DATE: 37-SEP-1996
FILING DATE: 37-SEP-1996
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1995
APPLICATION NUMBER: US 08/182,247
FILING DATE: 13-JAN-1994
ATTORREY/AGENT INFORMATION:
NAME: CATHERING, POLIZZI M
REFISERATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 40,130
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,581
                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & FORRSTER
STREET: 755 PAGE MILL ROAD
                      IN PROSTATE
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Patent No. 6136792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5836 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-08-891-581-1
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COUNTRY: U
ZIP: 77010
                         STATE: CA
COUNTRY: U
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US-08-611-587-1/c
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100.0%; Pred. No. 2.3e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8453;
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                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/09167681A

Sequence 45, Application US/09167681A

Patent No. 6265561

GENERAL INPORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Dianne M.
TITLE OF INVENTION: SULFORRANSERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 45
LENGTH: 8447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.5%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 6e-Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 3339
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bozicevic & Reed, LLP
LENGTH: 5836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
(6322)...(6447)
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US-09-167-681-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                       STRANDEDNESS: Sin
TOPOLOGY: linear
US-09-033-333-2
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US-09-167-681-45
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US-09-009-913-1
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept. STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 3;
Pred. No. 7.4e-11
                                                                                                                                 SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Sco. 100.0%; Pred. No. ...
285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,587
FILLING DATE: 03-MAR-1996
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MONTERMINI, LAURA
APPLICANT: MONTERMINI, LAURA
APPLICANT: MOLO, MARIA D.
APPLICANT: Koenig, Michael
APPLICANT: Campuzano, Victoria
APPLICANT: Cossee, Mireille
TITLE OF INVENTION: Direct Diagno
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08611587 Patent No. 6150091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEG
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: 650-327-3231
                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1. SEQUENCE CHARACTERISTICS: LENGTH: 72928 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-009-913-1
                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3
Best Local Similarity 100.
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                  Palo Alto
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STREET: Loc.
TTMY: Houston
                                                      USA
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us-09-813-492-1.oli.rni

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APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W 1fel, Thomas; Coulie, Pierre;
APPLICANT: Traversari, Catia; W 1fel, Thomas; Coulie, Pierre;
APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                            The sequence is preceded by an unsequenced portion of from 4.7 to 5.3 kilobases
                                                                                                                                                                                                                                                                                                                                                               Length 4129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                          Query Match 2.2%; Score 44; DB 2; Le Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. 6201111man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09224834; Patent No. 6201111; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12: SEGUENCE CHARATERISTICS:
LENGTH: 4129 base pairs
(212) 688-9200
                 TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS
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New York
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-370-319C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                      TOPOLOGY: linear
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US-09-224-834-12/c
  TELEPHONE:
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Betent No. 5856091

GENERAL INFORMATION:

APPLICANT: Brichard, Vincent; Van Pel, Aline;

APPLICANT: Traversari, Catia; W 1fel, Thomas; Coulie, Pierre;

APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne.

TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A

TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE T

TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%; Score 45; DB 3; L
100.0%; Pred. No. 2.3e-10;
tive 0; Mismatches 0;
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CLASSIFCATION 435
PRIOR APPLICATION A18:
APPLICATION NUMBER: 08/272,351
FILING DATE: 8-JULY-1994
PRIOR APPLICATION NUMBER: 08/032,978
APPLICATION NUMBER: 08/032,978
APPLICATION NUMBER: 08/032,978
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5856091man D.
RECISTRATION NUMBER: 30,946
RECISTRATION NUMBER: 10JD 5377.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319C
FILING DATE: 10-JANUARY-1995
CLASSIFICATION: 435
                             Sarah J.
                                                                     REFERENCE/DOCKET NUMBER: D-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5620
TELERA: 76-2829
INFORMATION FOR SEQ ID:
SEQUENCE CHARACTERISTICS:
LENGTH: 8353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                           NAME: Brashears-Macatee, Sa REGISTRATION NUMBER: 38,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 9q13
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.2%
Best Local Similarity 100.0
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NANTI-SENSE: NO
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; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
APPLICANT: Pan, Yano C.
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER PELICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
                                                                                                                                                                                   Gaps
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; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3 (OTHER INFORMATION: kilobases US-09-224-834-12
                                                                                                                                Query Match 2.2%; Score 44; DB 4; Length 4129; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 1169 tttttttttgagacagagtctcactctgttgcccaggctggagt 1212
                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

Location: (1)...(176373)

COTHER INFORMATION: n = A,T,C or G

US-09-128-155-17
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                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-128-155-17/c
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Search completed: October 7, 2002, 12:56:52 Job time: 6736 sec

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Human breast speci
Human secreted pro
         Human RinTinTin cD
Human MACK hybridi
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Human immune/haema
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Human reproduc
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AAL05517
AAL05518
AAK87363
AAK87360
AAK87354
AAK87355
AAK87354
AAK87354
                                                                          AAV38293
AAV38292
AAS81261
AAK75733
ABA18403
                                                                                                                                                                                                                              AAF97871
AAK86144
AAK86144
AAK79160
AAK79161
ABA08089
AAL76868
AAK77683
AAL7683
AAC30479
AAC30479
                                                                                                                                                                                                                                                                                                                                                    AAK77684
AAC21190
AAX98284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 56..439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV38291 standard; cDNA; 731 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human C-C chemokine DVic-1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0761071.
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56..121
/*tag= b
122..436
/*tag= c
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Homo sapiens.
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27-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence codes for human DNAX Vic-1 (DVic-1) (see AAW60649), a novel C-C chemokine. DVic-1 cDNA can be obtained from e.g. skin, epithelial or wound healing libraries by PCR amplification or by hybridisation. 2 ESTS (see AAV38292-33) were obtained from a human foetal heart library and a human osteoblast library. These show homology and are probably ESTS from a similar transcript. The chemokine motifs of these 2 ESTS were compared, and a consensus sequence was derived and confirmed as encoding DVic-1. The DVic-1 gene has been localised to human chromosome 9p13. An alternative longer transcript (see AAV38296) for human DVIC-1 is also disclosed. Also claimed is novel human DNAX Groin Wound expressed CC chemokine (DGWCC) (see AAW60649), as well as expression vectors and host cells. DVIC-1 and DGWCC play a role in the requiation or development of the contract of
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                                                                                                                                                                                                                      treating abnormal physiology or development, e.g. cancerous or degenerative conditions
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Pred. No. 1.2e-193;
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Modulating cell movement within the skin, useful for treating immunological skin conditions or diseases comprises administering T cell-attracting chemokine or vasoactive intestinal contractor chemokine
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                                                                                                                                                                                                                                                                                                                                                                Cutaneous T-cell attracting chemokine; CTACK; skin; cell movemen! migration; vasoactive intestinal contractor; Vic; GPR2; agonist; antibody; immunological condition; mutein; ds.
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Zlotník A;
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                                                                                                                                                                                                     Human G-protein coupled receptor GPR27 encoding cDNA SEQ ID NO:1.
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designated GPR27. GPR27 has antimidrobially analgesic, cytostatic, antidiabetic, ancectic, antiasthmatic, antiparkinsonian, cardiant, hypotensiave, diuretic, osteopathic, cerebroprotective, antidiabetic, antidiabetic, antidepressant, antidepressant, neuroleptic, nootropic and anticonvulsant activities, and can be used in producing vaccines and in gene therapy. The GPR27 protein and polynucleotide are useful for treating certain diseases or as vaccines against these diseases. These diseases include bacterial, fungal, proteins these diseases. These diseases include bacterial, fungal, proteozoan or viral (e.g. infections caused by HIV-1 or HIV-2) infections, pain, cancers, diabetes, obesity, anorexia, bulinia, asthma, parkinson's disease, acute heart failure, hypotension, hypertension, urinary cretention, osteoprorsis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders (e.g. anxiety, schizophrenia, manic depression, depression, delirium, dementia or mental retardation), or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's syndrome). The polynuchectide may also be used for chromosome
                                                           polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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                                                    upled receptor GPR27 polypeptides and polynucleotide
ss or for treating diseases, e.g. infections, pain,
retention, osteoporosis, stroke, psychotic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic reagent for detecting mutations in the associated gene.
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                                                                                                                                                                                                                                                                        present sequence encodes a human G-protein coupled receptor
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100.0%; Pred. No. 1.2e-193
ive 0; Mismatches 0;
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Matches 498; Conservative
                                                                                                                                                  neurological disorders
                                                                                       useful as vaccines or cancers, urinary reten
                                                           G-protein coupled
AAB69175.
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antificiammatory; antirheumatic; antiarchridic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anamiagenciant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
neuroprotective; antidepressan; nootropic; antidiabetic; cytostatic;
meuroprotective; antidepressan; nootropic; antidiabetic; inflammation;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancratitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autolumnunity;
qenetic disease; haematopoietic disorder; platelet disorder; asthma;
whrombocytopaenia; osteoporossis; severe combined immunodeficiency;
allergic rhinitis; disbetes; multiple sclerosis; depression;
Alzhelmer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                           ttcctgacatttctgcaagctttgtattttatatttccactttatagatgaggaaatttga 1830
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                                                                                                                                                                                   192 atgtcttggaggtgataatgggacacacagaggcactgagtctccataggttaaaatgcc 251
                                                                                                                                                                                                                                                                                  132 tcaggtggcaggtgtcctgggcctcctgctggctagtcccaagcggtggtgttgccagg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1951 aattttaaattaattaaccgtgataaccaacattaataaaagttaagataccaaaa 2006
                                                                    atgtcttggaggtgataatgggacacacagaggcactgagtctccataggttaaaatgcc
Human protein encoding cDNA sequence SEQ ID NO:255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH99420 standard; cDNA; 698 BP.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer-associated nucleic acid molecules (N) and proteins (P), where cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. Nand P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P carperession. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Chaditionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and ABB7789 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1471 agttgataccattgtgccattcctcttttggcctcttttttgtccatagaggcttcaaga 1530
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                                                                                                                                                                                                                                                            colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                              Human colon cancer antigen encoding cDNA SEQ ID NO:1184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birse CE,
                                                                 AAH34102 standard; cDNA; 643 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0157137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US26524
                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                  colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235357/24.
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Matches 534; Conserv
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                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                           AAH34102
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AAX40376 standard; cDNA; 383

(first

16-JUN-1999

AAX40376;

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AAM199166 to AAH99904 encode the human proteins given in AAM2525 to
AAM25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antihilammatory; antiheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiovascular; antianaemic; antiangeregant; heamostatic; vulnerary;
cardiovascular; antianaemic; antiangeregant; heamostatic; vulnerary;
antidiabetic; coteopathic; dermatological; antiallergic; antiasthmatic;
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
cantidabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidabetic; cytostatic; neuroprotective; antidepressant; nootropic;
antidatostics antidepressant; nootropic;
antidatostics associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis; viral, bacterial, HIV and fungal
infections, autoimmunity, genetic diseases, haematopoietic disorders,
costeoporosis, severe combined immunodeficiency, eczema, allergic
criminits, asthma, diabetes, cancer, multiple sclerosis, depression,
antiditics, asthma, diabetes, cancer, multiple sclerosis, depression,
            polypeptides, useful for
ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 698 BP; 172 A; 170 C; 188 G; 168 T; 0 other;
polynucleotides encoding
                                      treatment and diagnosis of e.g. cancer,
                                                                                                       English
                                                                                                 Page 411; 1217pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorders.
            Isolated
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                   Gaps
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                   ö
 Length 698;
                   Indels
                   ;
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Score 403; DB 22;
Pred. No. 7.3e-155;
                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                    20.0%;
99.6%;
                  503; Conservative
         Similarity
Query Match
Best Local S
                  Matches
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Length 383; Indels

18.9%; Score 382; DB 20; L 100.0%; Pred. No. 2.9e-146; iive 0; Mismatches 0;

Conservative

Matches 382;

88

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148 62 208

Query Match Local

Similarity

61

agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag

RESULT AAX40376

267

directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.

Sequence 383 BP; 101 A; 91 C; 104 G; 87 T; 0 other;

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human secreted proteins, and encode the proteins given in AAY153 to human secreted proteins, and encode the proteins given in AAY153 to AAY1679, respectively. The proteins given the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, thassue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activitys. The products activity in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for sequences.
                                                                                                                                                                      forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemoclactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids encoding human secreted proteins - obtained from libraries derived from liver, lung, large intestine, colon,
                                                                                                                                                        secreted protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lacroix B;
                                                                                                                 Human secreted protein 5' EST SEQ ID NO:163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 276-277; 398pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclert A, Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                            Homo sapiens.
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Homo sapiens
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                                                                                                                                                                                                                                                       Human GFRP-2; growth factor related molecule; breast tissue; breast tumour; CC chemokine; hTECK homologue; developmental disorder; cell proliferative disorder; immune disorder; reproductive disorder; cardiovascular disorder; bacterial infection; viral; fungal; parasitic; cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents cDNA encoding human growth factor related molecule GFRP-2. cDNA encoding GFRP-1 was initially identified in a breast tissue cDNA library, and the present sequence represents a consensus derived from several overlapping and/or extended cDNA clones. GFRP-2 is probably a CC chemokine and has chemical and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human growth factor related molecule protein useful for the diagnosis and treatment of disorders associated with its activity including developmental, cell proliferative, immune, reproductive and cardiovascular disorders and infections -
                327
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181
                                                  agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag
                  gctcctggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttggc
                         Baughn MR;
                                                                                                                                                                                                                                       cDNA encoding human growth factor related molecule GFRP-2.
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50..433
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                                                                                                                                        362 gaagaaacaccatggcaagagg 383
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99US-0313457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC
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Au-Young
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homology with hTECK (20% identity). GFRP-2 and hTECK are both basic proteins, having isoelectric points of 10.1 and 10.2, respectively. GFRP-2 was found by Northbarn analysis to be expressed in both tumorous and nontumorous breast tissue. GFRP proteins (AAB03000-B03003), nucleotides encoding them (AAA52455-A52458), GFRP agonists and antagonists may be used to treat a wide variety of diseases associated with increased or decreased expression or activity of GFRP proteins. Conditions which may be treated include developmental disorders, cell proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., manstrual cycle disorders) cardiovascular disorders (e.g., arteriosclerosis) and bacterial, viral, fungal or parasitic infections. Additionally, GFRP proteins and nucleotides can be used in the diagnosis of such disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 382; DB 21;
Pred. No. 2.8e-146;
); Mismatches 1;
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99.8%;
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Matches 432; Conserv
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              AAX89389
                                      The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conditional partners are useful human the sequence data for this patent did not appear in the printed sequence of the invention.
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                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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100.0%; Pred. No. 1.6e-127;
iive 0; Mismatches 0;
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                                                                                                                                                                                                            Claim 1; SEQ ID No 12362; 103pp; English
                                                                                    Tang YT;
30-MAR-2001; 2001WO-US08631
                        2000US-0540217
2000US-0649167
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                                                                                                           WPI; 2001-639362/73.
P-PSDB; ABG12371.
                                                                                    Drmanac RT, Liu C,
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es 336; Conserv
                                                             (HYSE-) HYSEQ INC
                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                     biodiversity
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Matches
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antibonic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antiponic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding cystitis, and benign hyperplasias as well as other malignancies. The present sequence represents the nucleotide sequence of the human mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A mammary associated chemokine and related polynucleotides, useful for detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                Chemokine; breast tissue; breast milk; breast disease; vaccine; liflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; ss.
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Xaa)
                                                                                                                                                        Human mammary associated chemokine (MACK) encoding cDNA.
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Pred. No. 3.4e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "MACK"
/note= "Xaa = unknown"
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  BP.
AAX89389 standard; cDNA; 3117
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                                                                                                    (first entry)
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116..430
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Best Local Similarity 100.C
Matches 313; Conservative
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detection and treatment of breast disease, especially cancer
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                                                                                                                                                          1874
                                                                                                                                                                                          876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammary associated chemokine and related polynucleotides, useful
                                                    tttgagtagctaccgttgtttggattgaaattttctgatactgaaaagaacaaaagcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mammary associated chemokine (MACK) open reading frame.
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/transl_except= (pos: 270..272, aa: Xaa)
/product= "MACK"
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98US-0071899.
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P-PSDB; AAY29092, AAY29093.
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20-JAN-1998;
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antigody that recognizes the novel chemokine, or a chemokine-derived antigonic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antigonic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine can samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding polynucleotides include inflammations, infections, mastitis, benign population hyperplasias as well as other malignancies. The present sequence represents the human mammary associated chemokine present sequence.
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Pred. No. 3.1e-104;
0; Mismatches 2;
Claim 20; Page 20; 76pp; English.
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larity 99.5%;
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nes 379; Conserv
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The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antigenic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a callular receptor for the chemokine, can also be used to treat breast disease. Antigenic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding polynucleotides include inflammations, infections, mastitis, benign cystitis, and benign hyperplasias as well as other malignancies. The present sequence represents an antisense riboprobe that hybridises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 tgctgtcatccttcatgtcaagcgcagaagaatctgtgtcagcccgcacaaccatactgt
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                                                                                                                                                                                                                                                                       A mammary associated chemokine and related polynucleotides, usef for detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human mammary associated chemokine (MACK) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 311 BP; 65 A; 77 C; 72 G; 95 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.0%; Score 202; DB 20; Best Local Similarity 99.3%; Pred. No. 8.4e-73; Matches 302; Conservative 0; Mismatches 2;
                                                                                                                                                                                            Papsidero LD;
                                                                                                                                                                                                                                                                                                                                 Claim 29; Page 26; 76pp; English.
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                                                                                                                                                     (CODO-) CODON DIAGNOSTICS LLC
                                                                                         98US-0092155.
98US-0071899.
                                                     99WO-US00651
                                                                                                                                                                                            Frustaci JM,
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                22-JUL-1999
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                                                                                                                                                                                                                                                                                                        Rin tin tin polypeptides and polynucleotides useful as a diagnostic tool and for treating and preventing various diseases e.g. autoimmune diseases, cancer, infections, bone disorders etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 aggotociggaaagagigaataigigicgcaiocagagagoigaiggggatigigactig 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a chemokine designated RinTinTin. The RinTinTin polynuclectide is useful as a diagnostic reagent through detecting mutations in the associated gene. The polynuclectide and polypeptide are useful for screening agonists and antagonists of RinTinTin and are also useful as vaccines in treating various diseases such as allergies, asthma, atheroscierosis, autoimmune disease, cancer, osteoarbhritis, various infections, psoriasis, rheumatoid arthritis, and vascular disease.
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Pred. No. 1.5e-80;
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 27; 30pp; English.
                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                         24-MAY-2000; 2000WO-US14197
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                                                                                                                                                                                                                                               WPI; 2001-061533/07.
P-PSDB; AAB50353.
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            WO200073447-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Absolug- and products dependent on DNA and amino acid sequences. Absolug- and products dependent on DNA and amino acid sequences. Absolug- and products dependent on DNA and and and an and approach and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                            encoding novel human diagnostic protein #17066.
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100.0%; Pred. No. 9.8e-69;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 17066; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
13-FEB-2002 (first entry)
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                                                                                                                                                                                                         Homo sapiens
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Matches 192;
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This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosing, monitoring, staging, imaging and treating breast cancer (BC). The methods comprise measuring the lavels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific genes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 BP; 52 A; 64 C; 70 G; 60 T; 7 other;
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.00.0%; Pred. No. 8.2e-64;
                                                                                                                                                                                                                                                                   Human breast specific gene LS clone 2299454
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100.0%; Pre-
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Best Local Similarity
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ID AAX5
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human secreted proteins, and encode the proteins given in AAY12681 to human secreted proteins, and encode the proteins given in AAY12681 to AAY12913, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, heamostation activity, heamostatic activity, heamostatic activity, heamostatic activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a
                                                                                                                                                         forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytckine activity; cell proliferation; differentiation; hacmatopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from testis, ovary, uterus and spleen tissue
                                                                                                                                          Human; secreted protein; EST; expressed sequence tag; diagnosis;
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                                                                                                  Human secreted protein 5' EST SEQ ID NO:235.
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                                                                                                                                                                                                                                                                                                                                                                                                          98WO-IB01231
                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0905279
                                                       (first entry)
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                                                         21-JUN-1999
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                   AAX51656;
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ö Gaps ; 0 Length 254; Indels . , 6.2%; Score 126; DB 20; 100.0%; Pred. No. 8.9e-42; Live 0; Mismatches 0; Best Local Similarity 100. Matches 126; Conservative Query Match

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Search completed: October 7, 2002, 12:56:06 Job time: 6456 sec

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4.5 Compugen Ltd. Search time 1711.15 Seconds (without alignments) 15909.393 Million cell updates/secataccaaaaaaaaaaaaaaaa 2017 sidues ters: 27472414	results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES SUMMARIES ID Description BE034600 BF034600 BF034600 BF034600 BF030240 BG530240 BG682175 BG682175 BG682175 BG682175 BG682175 BF088415 BE088415 BE088415 BE088415 BE463561 N030300 N030300 N030300 N030300 N030300 BG614513 N030300 BG614513 N030300 BG614513 N030300 BG614513 BG532385 BG532385 BG633385 BG732385 B	R38459 YH89d12.rl BE004848 MR2-BN011
GenCore version 4 Copyright (c) 1993 - 2000 c Cleic search, using sw model October 7, 2002, 09:36:05; US-09-813-492-1 2017 1 tagatacctgaacacctcc OLIGO_NUC Gapop 60.0, Gapext 60.0 13736207 seqs, 6748477542 res 0 hits satisfying chosen paramet length: 0 length: 2000000000 Listing first 45 summaries	EST:* : em_estba:* 3: em_esthum:* 4: em_esthum:* 5: em_estcov:* 6: em_estcov:* 6: em_estpl:* 7: em_estpl:* 10: gb_est1:* 11: gb_htc:* 11: gb_htc:* 11: gb_htc:* 11: gb_htc:* 11: gb_htc:* 12: gb_ess_hum:* 14: em_gss_hum:* 15: em_gss_hum:* 16: em_gss_hum:* 17: gb_est1:* 18: fb em_gss_hum:* 18: fb em_gss_hum:* 19: fb em_gss_hum:* 19: fb em_gss_hum:* 10: fb em_gss_hum:* 10: fb em_gss_hum:* 11: fb em_gss_hum:* 12: fb em_gss_hum:* 13: fb em_gss_hum:* 14: fb em_gss_hum:* 15: fb em_gss_hum:* 16: fb em_gss_hum:* 17: fb em_gss_hum:* 18: fb em_gss_hum:* 19: fb em_gss_hum:* 10: fb em_gss_hum	6.8 417 10 6.0 510 9
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GEAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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60255934BF1 NIH_MGC_61 Homo sapiens CDNA clone IMAGE:4697338 5',
MRNA sequence.
                                                                                                                                                                                                                                                                       /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
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100.0%; Pred. No. 2.8e-142;
ive 0; Mismatches 0;
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/tissue_type="serous papillary
pooled tumors"
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1 (bases 1 to 508)
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National Cancer Institute, Cancer Genome Anatomy Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., P.
Emmert-Buck, M.D., Ph.D.
                                                 Length
                                             Score 567; DB 10;
Pred. No. 5.1e-160;
0; Mismatches 1;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4754250"
/clone_lib="NCI_CGAP_Skn4"
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Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Pases I to 869;

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capbs-remail nih.gov

Tissue Iprocurement: ATCC

CONA Library Preparation: CLONETECH Laboratories, Inc.

CONA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M. A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM1525 row: p column: 11

High quality sequence stop: 748.

Incelling all incompanies and insert size 1.75 kb (range on cloning as follows: 5'

Chone: Inbelling (The Mas prepared from cell line RNA. 5'

Mobile-stranded CDNA was prepared from cell line RNA. 5'

Sadaptors sequence: 5'-CACGCCCATTATGCCC-3' and 3' adaptors sequence: 5'-CACGCCCATTATGCC-3' 
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816 bp mRNA linear EST 01-MAY-2001 mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMLOGIS row: c column: 19
High quality sequence stop: 766.
627
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99.7%; Pred. No. 3.6e-116;
iive 0; Mismatches 0;
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1 (bases 1 to 450)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Leh,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco.
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                                                                                                              AI880389 455a07.xl Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2375892 3', mRNA sequence.
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/db_xref="taxon:9606"
/clone="INAGE:2375892"
/clone="INAGE:2375892"
/sex="maie"
/dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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AI880389.1 GI:5554438
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BE748488 11-SEP-2000 801571978F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838987 5',
                                                                       3']; double-stranded cDNA was ligated to Eco R1 adaptors [5' AATTCACTAGTAAT 3' and 5' ATTACTAGG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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1 (bases 1 to 873)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Stausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC.

CONA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                         Gaps
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/lab_host="DH10B (phage resistant)"
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Pred. No. 1.1e-109;
0; Mismatches 1;
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99.8%;
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Matches 449; Conservative
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BE748488
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Briones, M.R.,

expressed

Paulo-SP,

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Br0687"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=CMO-BT0687-210 300-297-f08&t3=2000-03-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stope: 399.
           Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccatcgtggccttggctgtctgtgcggccctacatgcctcagaagccatacttcccattg
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                      Shotgun sequencing of the human transcriptome with ORF sequence tags sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                             18.7%; Score 377; DB 10; I
100.0%; Pred. No. 2.3e-103;
Live 0; Mismatches 0;
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TGGACTTGGCCATGATT 449
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284 204 344 264 404 324 464 384

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Do 577)

E Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlifia, T., Soares, M., Tan, F., Trevaskis, E., Waterston

Rifkin, L., Wohlidman, P. and Wilson, R.

The Washu-Merck EST Project

I Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Gev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I: Site_2: Eco RI:
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGATTAATTATTTTTTTTTTT],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

58 a · 135 c 132 g 141 t lothers
                                                                                                                                                                                           N63913 5227h10.s1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone INMGE:29387 3' similar to contains element MIR repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 356.
Location/Qualifiers
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84 GACTIGCCCAGGICACACAGGAAGIGGCAGAGACAAGCITITIAAAITAAGAAAAAITAA
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100.0%; Pred. No. 6.6e-77;
tive 0; Mismatches 0;
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                                      ;, mRNA sequence.
N63913
N63913.1 GI:1211742
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Matches 289;
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/note=="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_GGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Falima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
Seq primer: -400P from Gibco.
                                                                                BE463561 362 bp mRNA linear EST 27-JUL-2000 hw25b05.xl NCI_CGAP_Kid11 Homo sapiens CDNA clone IMAGE:3183921 3',
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NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 3.5e-87;
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/clone="IMAGE:3183921"
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The Washu-Marck EST Project
Contact: Wilson RK
Washington University School of Medicine
4444 Porest Park Parky, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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                                                                                                                                                                                                      N98285 10-APR-1996 a227hl0.rl Soares fetal liver spleen lNFLS Homo sapiens.cDNA clone IMAGE:293827 5' similar to contains Alu repetitive element;, mRNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop:
Location/Qualifiers
1. 437
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/db_xref="GDB:3801674"
/db_xref="taxon:9606"
/db_axref="taxon:9606"
/clone="THAGE:293877"
/clone=lib="Soares fetal liver spleen lNFLS"
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                                                                                                   /sex="male"
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Length 1066; Indels

Length 472;

12.6%;

Query Match

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N27569 487 bp mRNA linear EST 30-DEC-1995
yx43b10.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:264475 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 303
Source: IMAGE Consortium, Linu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infodimage.llnl.gov) for further information.
Insert Length: 541 Std Error: 0.00
Seq primer: T7
High quality sequence stop: 303.
High quality sequence stop: 303.
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlifing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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/sex="Male"
                                                           9.6%; Score 194; DB 10;
100.0%; Pred. No. 9e-49;
Live 0; Mismatches 0;
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/db_xref="GDB:3874117"
/db_xref="taxon:9606"
/clone="IMAGE:264475"
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N27569.1 GI:1142050
                                                             Query Match 9.6'
Best Local Similarity 100.'
Matches 194; Conservative
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/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="lib="NIH_MGC_61"
/clone="lib="NIH_MGC_61"
/clone="lib="NIH_MGC_61"
/clone=lib="NIH_MGC_61"
/lab_host="bH108 (T1 phage=resistant)"
/lab_host="DH108 (T1 phage=resistant)"
/note="Organ: testis: Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccattaggcc); Site_2: Sfil (ggccattaggcc);
Sfil (ggccattaggcc); Site_2: Sfil (ggccattaggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGAGGCGGCGCGCATG-T(3)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.94.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG614513 1066 bp mRNA linear EST 18-APR-2001 602642663F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773711 5',
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National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
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Pred. No. 2.2e-66;
            100.0%; Pred. ...
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                        M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 112 c 109 g 147 t 5 others
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constructed by Bento Soares and
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http://image.llnl.gov
Plate: LLCM1532 row: g column: 23
High quality sequence stop: 729.
Location/Qualifiers
1. 798
                                                                                                                                                                                                                                9.5%; Score 191; DB 10;
99.6%; Pred. No. 1.4e-47;
tive 0; Mismatches 1;
   (Pharmacia). Library
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BG532385.1 GI:13523923
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
    Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Rechnologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bi.llnl.gov/bbry/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 285.
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Normalized to Cot 50. Average insert size 1.32kb.
Normalized version of NCI_CGAP_Co18. Library constructed
by Life Technologies."
13 c 1 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR: This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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100.0%; Pred. No. 1e-33;
tive 0; Mismatches 0;
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Human Human

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Chemokine; breast tissue; breast milk; breast disease; vaccine; human; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; ss.
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    /*tag= b
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Compugen Ltd.
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
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                                                                                                                                                                                                                              The invention provides an isolated human chemokine, which is preferentially expressed in breast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antibodive that recognizes the novel chemokine, or a chemokine-derived antibodic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antiponic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding cystitis, and benign hyperplasias as well as other mailgnancies. The present sequence represents the nucleotide sequence of the human mammary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              immary associated chemokine and related polynucleotides, useful detection and treatment of breast disease, especially cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttgtgatcaaattcaggtttaatgtttttggttaagaatttcctacgtgaattcgtgtac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Length 3117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3117 BP; 860 A; 582 C; 566 G; 921 T; 188 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.3%; Score 1035.2; DB 2
86.5%; Pred. No. 5.7e-206;
11ve 73; Mismatches 92;
                                                                                             Dyster LM, Frustaci JM, Papsidero LD;
                                                                                                                                                                                                       Claim 19; Page 18-20; 76pp; English
                                                                  (CODO-) CODON DIAGNOSTICS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine (MACK).
 99WO-US00651
                         98US-0092155
98US-0071899
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Matches 1172; Conservative
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12-JAN-1999;
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                                             tctcttgcctcagcct-cccaagtaactgatattacaggcgcccagccaccaccccgc 1324
                                                                                                                                                                                                                                                                                                                                               ag-tgcagtggcacaatctcggct-cattgcaacctccgcctcccg--cgttcaagtgat
                          tatttatattttccactttatagatgaggaaatttgaggctcttagaggtaaaatgacttg
                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer antigen encoding cDNA SEQ ID NO:1184
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Homo sapiens.

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1820 aggaaatttgaggctcttagaggtaaaatgacttgcccaggtcacacaggaagtggcaga
                        1880 gacaagctttttaaataagaaaaattaataaaaatataagagtaacttaaaaatat
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                                                                                                                                                                                                                                                        AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, and angains and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inscribing the nucleic acids into a host cell and culturing the cell of express the proteins. N and P can be used in the prevention, diagnosis and AAR77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 643 BP; 210 A; 117 C; 116 G; 198 T; 2 other;
                                                                                                                                                  Rosen CA;
                                                                                                                                                                                                                                         Claim 1; Page 2980-2981; 9803pp; English
                                                                                                                                                 Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.9%;
99.1%;
                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                        99US-0157137.
                                                                  28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.1
Matches 544; Conservative
                                                                                                                                               Ruben SM, Barash SC,
                                                                                                                                                                      2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.
N.B. Pages 666 to
                                                                                                                                                                                   P-PSDB; AAG74697
                     WO200122920-A2.
                                                                                         29-SEP-1999;
                                                                                                   03-NOV-1999;
                                           05-APR-2001
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antific Lammatory; antirheumatic; antiarthritic; immunosupressive;
w antibacterial; endocrine; cardiant; central nervous system; virucide;
w antibacterial; endocrine; cardiant; central nervous system; virucide;
w antiaggregant; heamostatic; vulnerary; antiulcer; osteopathic; eczema;
w dermatological; antiallergic; antiathmatic; antidiabetic; cytostatic;
n europrotective; antidepressant; nootropic; antidiabetic; cytostatic;
n munostimulant; gene therapy; antisense therapy; vaccine; inflammation;
w miniamphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoletic disorder; platelet disorder; asthma;
w thromboytopeania; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; disbetes; multiple sclerosis; depression;
w Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
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The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; anti-HIV; fungicide; antimutagen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein encoding cDNA sequence SEQ ID NO:255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 411; 1217pp; English.
                   BP
AAH99420 standard; cDNA; 698
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antidabetic; cytostatic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cartiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumactol arthritis, septic shock, pancreatitis, cardiac dysfunction, renuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, agenetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodefliciency, eczema, allergic hintits, asthma, diabetes, cancer, multiple sclerosis, depression, allergine, and participal and antipal sclerosis, depression, allergine, and participal and antipal sclerosis, depression, allergine, and antipal sclerosis, depression, and antipal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 501.8; DB 22; 99.6%; Pred. No. 3.5e-95; ive 0; Mismatches 2;
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Best Local Similarity 99.6'
Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                                                                           neurological disorders.
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This cDNA sequence codes for human DNAX Vic-1 (DVic-1) (see AAW60649),
a novel C- Chemokine. DVic-1 cDNA can be obtained from e.g. skin,
epithelial or wound healing libraries by PCR amplification or by
copital control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 ctgatcgaacagcetcaettgtgttgetgtcagtgccagtagggcaggcaggaatgcage 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVic-1 and DGWCC chemokines - useful for developing products i
treating abnormal physiology or development, e.g. cancerous or
degenerative conditions
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Pred. No. 2.2e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vicari A, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 59-60; 71pp; English.
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           96US-0761071
96US-0031805
                                                                                                                                                                                                                                                                                                                    97WO-US21092
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56..121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hedrick JA, Morales J,
                                                                               56..439
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P-PSDB; AAW60649.
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                                                                                                                           sig_peptide
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Human; G-protein coupled receptor; GPR27; antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian; cardiant; hypertensive; hypotensive; diuretic; osteopathic; antiulicer; cerebroprotective; antialler; anticlemetic; tranquilliser; nootropic; antidepressant; neuroleptic; anticonvulsant; vaccine; gene therapy; infection; pain; cancer; diabetes; obesity; anorexia; bulimia, asthma; Parkinson's disease; acute heart failure; hypotension; hypertension;
                                          Modulating movement of a cell within or to the skin of a mammal can be achieved by administering an antegonist or agonist of cutaneous T cell-attracting chemokine (CTACK) or vasoactive intestinal contractor (Vic) chemokine. The antegonist is selected from a mutein of natural CTACK or Vic, an antibody which neutralises CTACK or Vic or an antibody which plock GPR2 ligand binding. The CTACK or Vic agonists or antagonists are useful for treating medical conditions or diseases associated with immunological conditions of the skin.
                                                                                                                                                                                                                                                                                                         agagagactcgccatcgtggccttggctgtctgtgcggccctacatgcctcagaagcca 122
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                                                                                                                                                                                            Sequence 731 BP; 206 A; 193 C; 163 G; 168 T; 1 other;
                                                                                                                                                                                                                                         Score 498; DB 21;
Pred. No. 2.2e-94;
0; Mismatches 0;
               Page 68-69; 79pp; English.
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tacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaaggctcc 182
                                                                                                                                                                                                                           aacaccatggcaagaggaacagtaacagggcacatcaggggaaacacgaaacatacggcc 512
                                                                                                                                                                                                                                                                                                             Cutaneous T-cell attracting chemokine; CTACK; skin; cell movement; migration; vasoactive intestinal contractor; Vic; GPR2; agonist; antagonist; antibody; immunological condition; mutein; ds.
                              tggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttggctgctg
                                                             tggaaagagtgaatatgtcgcatccagagagctgatggggattgtgacttggctgctg
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Zlotnik A;
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Kellermann S, McEvoy
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urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic disorder; neurological disorder; dyskinesia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present sequence encodes a human G-protein coupled receptor
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                                                                                                                                                                                                                                                                                  99US-0361564.
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Human GFRP-2; growth factor related molecule; breast tissue; breast tumour; CC chemokine; hTECK homologue; developmental disorder; cell proliferative disorder; immune disorder; reproductive disorder; cardiovascular disorder; bacterial infection; viral; fungal; parasitic; cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis; consensus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and treatment of disorders associated with its activity including developmental, cell proliferative, immune, reproductive and cardiovascular disorders and infections
                                                                                            agtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgtttgccacaggaaga 369
                                                                                          512
                                                                                                                                       572
                                                                                                                                                   This sequence represents cDNA encoding human growth factor related molecule GFRP-2. cDNA encoding GFRP-1 was initially identified in a breast tissue cDNA library, and the present sequence represents a
                                               ataaaactccttattagagagtctacagataaatctacagagacaattcctcaagtggac
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                                                                                                                                                                                                                                                                                                                                     cDNA encoding human growth factor related molecule GFRP-2.
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/product= "Human GFRP-2"
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consensus derived from several overlapping and/or extended cDNA clones. GFRP-2 is probably a CC chemokine and has chemical and structural homology with hTECK (20% identity). GFRP-2 and hTECK are both basic proteins, having isoelectric points of 10.1 and hTECK are both basic and nontumorous breast tissue. GFRP proteins (AAB3000-B0303), nuclectides encoding them (AAA52455-A5248), GFRP agonists and antagonists may be used to treat a wide variety of diseases associated with increased or decreased expression or activity of GFRP proteins. Conditions which may be treated include developmental disorders, cell proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., menstrual cycle disorders) cardiovascular disorders (e.g., arteriosclarosis) and bacterial, viral, fungal or parastic infections. Additionally, GFRP proteins and nucleotides can be used in the diagnosis of such disorders.
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                        Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #12362.
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                                                                                                                                                                                                                                                                                                      Score 441; DB 21;
Pred. No. 1.5e-82;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                      Match 21.9%;
Local Similarity 96.0%;
les 485; Conservative
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymoclecitides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. AAS04197-AAS04564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gotcot-ggaaagagtgaatatgtgtcgcatccagagagagtgatggggattgtgactt-g 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag
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Pred. No. 1.2e-81;
. --+-hes 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 12362; 103pp; English.
                                                                                                                                                                                                                                                      Tang YT,
                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                    31-MAR-2000; 2000US-0540217
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Matches 487; Conservative
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                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73
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                                  WO200175067-A2.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
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                                                        561
                        681
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                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                        aacatacggccataaaactccttattagagagtctacagataaatctacagagacaattc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #17066
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                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                           AAS81262 standard; cDNA; 474
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23-AUG-2000; 2000US-0649167.
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forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                             263
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                                                                                                                                                               Indels
                                                                               Sequence 474 BP; 134 A; 112 C; 124 G; 104 T; 0 other;
                                                                                                                   .8; DB 23;
4.4e-76;
diagnostic coding sequences of the invention Note: The sequence data for this patent did
                                                                                                                             Score 409.8; I
Pred. No. 4.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST SEQ ID NO:163.
                                                 at ftp.wipo.int/pub/published_pct_sequences
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97.3%;
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                                                                                                                                                Best Local Similarity 97.3 Matches 460; Conservative
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                                                                                                                           human secreted proteins, and encode the proteins given in AAY1531 to human secreted proteins, and encode the proteins given in AAY11533 to human secreted proteins, and encode the proteins given in AAY11533 to AAY11679, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for disponsis and therapy. The proteins obtained may have cytokine activity, call proteins obtained may have cytokine activity, call proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell.
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                                                                New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from liver, lung, large intestine, colon,
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100.0%; Pred. No. 2.5e-70;
cive 0; Mismatches 0;
           Lacroix B;
                                                                                                        Claim 1; Page 276-277; 398pp; English.
           Dumas Milne Edwards J,
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                                                                                     thyroid and pancreas tissue
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Best Local Similarity 100.
Matches 382; Conservative
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           Duclert A,
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                                                           vaccine; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Xaa = unknown; the start and stop codons
                                          Chemokine; breast tissue; breast milk; breast disease; vaccine; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; ss.
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Human mammary associated chemokine (MACK) open reading frame.
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                                                                                                                                                                                                                                                                                                                                          /codon_start= 3
/transl_except= (pos: 207..209, aa: Xaa)
/transl_except= (pos: 270..272, aa: Xaa)
/product= "MACK"
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69..378
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P-PSDB; AAY29092, AAY29093.
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Best Local Similarity 99.5
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          386
                                                                                                                DVic-1; DNAX Vic-1; C-C chemokine; cytokine; human; immune system; cancer; cell proliferation; therapy; diagnosis; HHFFQ25R; ss.
                                               aagccatacttcccattgcctccagctgttgcacggaggtttcacatatttccagaa
                                      ggctcctggaaagagtgaatatgtgtcgcatccagagagctgatggggattgtgacttgg
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                                                                                                                                                                                                                                                                                                                         Human C-C chemokine DVic-1 EST HHFFQ25R
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Chemokine; breast tissue; breast milk; breast disease; vaccine; human; inflammation; infection; mastitis; benign cystitis; hyperplasia; mammary associated chemokine; MACK; probe; ss.
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including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. Abnormal proliferation, regeneration, degeneration, and atrophy may be modulated by appropriate therapeutic treatment using products of the invention. The procan also be used for detection, diagnosis and drug screening.
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Pred. No. 1e-67;
0; Mismatches 70;
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Best Local Similarity 85.0%;
Matches 420; Conservative (
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                                                                                                                                                                   preferentially expressed in preast tissue or detected in breast milk. An antibody that recognizes the novel chemokine, or a chemokine-derived antibody that recognizes the novel chemokine, or a chemokine-derived antigenic peptide, can be used to treat breast disease in a patient. A peptide, which binds to a cellular receptor for the chemokine, can also be used to treat breast disease. Antigenic peptides of the chemokine can be used to vaccinate patients against breast disease. The chemokine polynucleotide sequences and the chemokine protein can be detected in samples with primers, probes and antibodies using standard techniques. This is useful for detecting breast disease. Other breast diseases that may be treated or detected with the chemokine and its encoding polynucleotides include inflammations, infections, mastitis, benign eystitis, and benign hyperplasias as well as other malignancies. The present sequence represents an antisense riboprobe that hybridises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agccatacttcccattgcctccagctgttgcacggaggtttcacatcatatttccagaag 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AGCCATACTTCCCATTGCCTCCAGCTGTTGCACGGAGGTTTCACATCATATTTCCAGAAG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mammary associated chemokine and related polynucleotides, useful or detection and treatment of breast disease, especially cancer
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                                                                                                                                                           provides an isolated human chemokine, which is
                                                                                                                                                                                                                                                                                                                                                                                Length 311;
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                                                                                                                                                                                                                                                                                                                        the human mammary associated chemokine (MACK) DNA
                                                                                                                                                                                                                                                                                                                                               Sequence 311 BP; 65 A; 77 C; 72 G; 95 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                Score 302; DB 20;
Pred. No. 1.1e-53;
0; Mismatches 2;
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                                                       Frustaci JM, Papsidero LD;
                                                                                                                                   Claim 29; Page 26; 76pp; English.
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                                 DIAGNOSTICS LLC.
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Best Local Similarity 99.3%;
Matches 302; Conservative
98US-0092155.
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                                                                                                                                                           The invention
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09-JUL-1998;
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                                                       Dyster LM,
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DVic-1; DNAX Vic-1; C-C chemokine; cytokine; human; immune system;

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This sequence defines EST HOEDHIIR obtained from a human osteoblast
library. It shows high homology to EST HHFFQ25R (see AAV38292)
cobtained from a human foctal heart library. The two ESTS are
probably from a similar transcript. The chemokine motifs of the
two ESTS were compared, and a consensus sequence was derived and
subsequently confirmed as encoding human DNAX Vic-1 (DVic-1) (see
AAW60649), a novel C-C chemokine. CDNA (see AAV38291) encoding DVic-1
can be obtained from e.g. skin, epithelial or wound healing
libraries. DVic-1 plays a role in the regulation or development of
neuronal or haematopoietic cells, e.g. lymphoid cells, which affect
immunological responses. It can be used in the treatment of
conditions associated with abnormal physiology or development,
including abnormal proliferation, e.g. cancerous conditions or
degenerative conditions. Abnormal proliferation, regeneration,
degeneration, and atrophy may be modulated by appropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 cctcagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcatattt 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating abnormal physiology or development, e.g. cancerous or degenerative conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can also be used for detection, diagnosis and drug screening.
cancer; cell proliferation; therapy; diagnosis; HOEDH11R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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88.8%; Pred. No. 3.2e-45;
                                                                                                                                                                                                                                                                                                                                                                        Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic treatment using products of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 61-62; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Vicari A,
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96US-0031805
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                                                                                                                                                                                                                                                                                                                         (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-322730/28.
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                                                 Homo sapiens.
                                                                                              WO9823750-A2
                                                                                                                                                                                              26-NOV-1997;
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27-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                        Hedrick JA,
                                                                                                                                               04-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a breast specific gene (BSG) clone. The BSG sequences are also referred to as breast specific markers (BSM). The invention relates to methods for diagnosting, monitoring, staging, langing and treating breast cancer (BC). The methods comprise measuring the levels of BSG products in cells, tissues or body fluids of the patient and comparing the measured levels of BSG, with BSG levels of a normal human control. An antibody against the BSG sequences can be labelled and used for imaging BC in a patient. The antibody can be conjugated to a cytotoxic agent, and used for treating BC in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating breast cancer using protein product of breast specific genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                               Human; breast specific gene; breast specific marker; BSG; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 253 BP; 52 A; 64 C; 70 G; 60 T; 7 other;
                                                                                                                                                                      Human breast specific gene LS clone 2299454.
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                                                                                        AAZ91767 standard; DNA; 253 BP.
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558 attcc 562
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                        437 ttccc 441
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_pln:* em_gss_vrt:*

em_estba:*
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Database :

SUMMARIES

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f	at a	BG682175	BF034600	N63913	AW469978	BG530240	BG532385	AI880389	BG614513	BE748488	N98285	BE088415	N20300	BE463561	AZ575795	BE004848	N27569	BB617469
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Query	March	36.4	31.6	26.3	25.2	24.7	22.5	22.2	21.5	20.8	19.3	18.7	17.9	17.9	14.9	14.5	14.1	14.0
9	arore	734.2	638.2	530.2	508	497.8	454.2	448.4	434	418.6	389.2	377.2	361.8	360.4	301	292.6	283.4	281.8
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BB661838 BB661838 BF785656 602112060 BG749748 602119883 BE150796 RC2-HT027 BG493959 602542239 B59854 CIT-HSP-345 BG527374 602557360 BF712465 601813237 BF784128 601843165 BG777306 602664547 BG741134 602611696 R34459 yh89412.r1 BE062476 QV4-BT025 BF18498 601843479 BF18498 601843479 BG500685 602547078 BG7449 CIT-HSP-422 BG528312 60243790 BG776604 602663748 AQ17821 PG7 HSP-422 BG77861 BS748652 BF663361 602147612 BF663361 602147612 BF663361 602147612 BF663361 602147612 BF663361 602147612 BGC11712 HOMO SAP1	8	o mRNA linear EST 01-MAY-2001 sapiens cDNA clone IMAGE:4754250 5',	Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo. '//, Mammalian Gene Collection (MGC)	Syfunc. Cleaver, M.D. Life Technologies, Inc. The I.M.A.G.E. Consortium (LLNL) clone distribution information can be clone distribution information can be column: 19 pp: 766.	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="Index:4754250" /clone=lib="NCI_CGAP_SKN4" /tissue_type="Squamous cell carcinoma" /tab_host="DH10B (T1 phage-resistant)" /note="rogan: skin; Vector: pCMV-SPORT6; Site_1: NotI; /note="salI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." 84 a 199 c 172 g 261 t
BB661838 BF785556 BG249748 BG249359 BG249359 BG249359 BF212465 BF212465 BF777306 BF7	ALIGNMENT	816 bp Skn4 Homo s 572	thordata; Cr rimates; Ca i.nih.gov/. of Health, M	Email: cgapbs r@mail.nih.gov Tissue Procurement: James Cleaver, M.D. CDNA Library Preparation: Life Technol CDNA Library Arrayed by: The I.M.A.G.E DNA Sequencing by: Incyte Genomics, In Clone distribution: MGC clone distribu http://image.linl.gov Plate: LiAM10615 row: c column: 19 High quality sequence stop: 766. Location/Qualifiers 1. 816	tomo sapiens xxon:9606" ms:4754250" NCI_CGAP_S0" mol_CGAP
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                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: DoTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lette://image.llnl.gov
http://image.llnl.gov
plate: LLAMS591 row: o column: 05
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection
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Pred. No. 3.1e-85;
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                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                          Length 816;
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                                          10;
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Pred. No. 1.9e-99;
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                                        36.4%;
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DEFINITION

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Entargonic Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 508)

NoT-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (GGAP),

Tumor Gene Index

In Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Fissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW469978 508 bp mRNA linear EST 24-FEB-2000 xz27all.xl NCI_CGAP_Ut4 Homo sapiens CDNA clone IMAGE:2761340 3',
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                                                                                                                                                                                                                                                                  1566 ccaatagagagcaggagccactttatcaggtggcaggtgtcccgggcctccctgctggct 1625
                                                                                                                                                                                                                                                                                                                                             1626 agtcccaagcggtggtgttgccaggatgtcttggaggtgataatgggacacacagaggca 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CTGAGTCTCCATAGGTTAAAATGCCACCAAAACTGGCCTTTGCCTAATATCCCTCATTGA 153
                                     572 TITIGNATITITAGIAGAGGGTITITCCCCACGITGGCCGGGCTGGICTCAAACTCTT 513
                                                                                                               tttttgtccatagaggcttcaagatagataggtaagagcccagtagtgttcataagaag-
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Location/Qualifiers 1..508
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., William, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikin, L., Robhling, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
L. Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Emmal: est Wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lange.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                      N63913 577 bp mRNA linear EST 01-MAR-1996 za27h10.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:293827 3' similar to contains element MIR repetitive element
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               1329 ttttgtatttttagtagagacggggttttcccacgttggccgggctggtctcaaactct 1388
                                                                                             ttaaataagaaaaaattaataaaaatataataagagtaacttaaaatattaataaacca 1949
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/organism="Homo sapiens"
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High quality sequence stop: 356.
Location/Qualifiers
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illarity 98.8%;
Conservative
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N63913
N63913.1 GI:1211742
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human.

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL

COMMENT

FEATURES

AUTHORS REFERENCE

DEFINITION

N63913/c LOCUS

RESULT

959 1950

168

BASE COUNT

Matches 565; Query Match

Best Local

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Best Local Similarity 99.6
Matches 499; Conservative
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60255948F1 NIH_MGC_61 Homo sapiens cDNA clone IMACE:4697338 5',
BG530240
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                                                   /lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
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                                                                                                                                                                                                                                                                                  ttcataagaagccaatagagagcaggagccactttatcaggtggcaggtgtcccgggcct 1614
/clone="IMAGE:2761340"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade,
pooled tumors"
                                                                                                                                                                                                                                                                                                TATTTATATTTCCACTTTATAGATGAGGAAATTTGAGGCTCTTAGAGGTAAAATGACTTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 508;
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                         Query Match 25.2%; Score 508; DB 9; I
Best Local Similarity 100.0%; Pred. No. 6.2e-66;
Matches 508; Conservative 0; Mismatches 0;
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/done="Infatacon:good"
/clone="Infatacon:good"
/clone="Infatacon:good"
/clone=Infatacon:good"
/tissue_type="embryonal ractionma"
/lab_host="embryonal ractionma"
/lab_host="DH100 (T] phage-resistant)"
/note="Organ: testis: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Souble-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGGGCGCATG-T(30)BN-3'
(Where B = A, C, or G and N = A, C, G, Or T). Average
insert size 1.75 kb (range 0.94.0 kb): 15/15 colonies
contained inserts by PCR: This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCNESS row: p column: 11
High quality sequence stop: 748.
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    869
/organism="Homo sapiens"
/db_xref="taxon:9606"

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AI880389 450 bp mRNA linear EST 23-AUG-1999 at55a07.xl Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE22375892 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Glaco.
Location/Qualifiers
                                                                                        619
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Pred. No. 4.2e-57;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="IMAGE:2375892"
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Best Local Similarity 99.8
Matches 449; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Homo.

Expect Eutheria; Primates; Catarrhini; Hominidae; Homo.

RS NIH-WGC http://mgc.nci.nlh.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Streausberg, Ph.D.

Cond distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

http://image.llh.gov

Clone distribution: MGC clone distribution information can be http://image.llh.gov

Plate: LLCM153 row; g column: 23

High quality sequence stop: 729.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

//Lissue_type="membryonal carcinoma"

//Lissue_ty
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                                                                                     BG532385 198 bp mRNA linear EST 03-APR-2001 602561892F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699822 5',
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Pred. No. 4.6e-58;
0; Mismatches 8; Indels
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Best Local Similarity 97.8%;
Matches 492; Conservative
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BE748488 873 bp mRNA linear EST 15-SEP-2000 601571978F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838987 5',
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 873)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC
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95.1%; Pred. No. 3.9e-55;
iive 0; Mismatches 20;
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El (bases I to 1066)

Is I (bases I to 1066)

Is NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: CLONETECH Laboratories, Inc.

CONA Library Preparation: CLONETECH Laboratories, Inc.

CONA Library Preparation: CLONETECH Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLCM1645 row: n column: 16

High quality sequence stop: 613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602642663F1 NIH_MGC_61 Homo sapiens CDNA clone IMAGE:4773711 5', mRNA sequence.
BG514513
BG514513.1 GI:13665884
EST.
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/lab.host-"DH108 (T1 phage-resistant)"
/note="Corgan: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sf11 (ggccgcctggcc); Site_2: Sf11 (ggccattatggcc);
Double stranded cDNA was prepared from cell line RNA. s' and 3' adaptors were used in cloning as follows: 5'
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/db_xref="taxon:9606"
/clone="IMAGE:4773711"
/clone_lib="NIH_MGC_61"
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                                                                                                                                                /organism="Homo sapiens"
/db_xref='taxon.9606"
/clone='InAce:3838987"
/clone='InAce:3838987"
/clone_lib="NIH_MGC_55"
/tissue_type="from acute myelogenous leukemia"
/lab_host="blu108 (Ti phage-resistant).
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_l: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); plouble-stranded cDNR was prepared from cell line RNA.
); bouble-stranded cDNR was prepared from cell line RNA.
); adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCAGCATG-dT(30)BN' 3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by clontech
Laboratories (Palo Alto, CA)."
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              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. k column: 20
High quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 atactgttaagcagtggatgaaagtgcaagctgccaagaaaaatggtaaaggaaatgttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gccacaggaagaaacaccatggcaagaggaacagtaacaggggcacatcaggggaaacacg
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 418.6; DB 1
Pred. No. 8.1e-53;
0; Mismatches 14
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RESULT N98285

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l. 437
/organism="Homo sapiens"
/db_xxef="c0bis:3801674"
/db_xxef="c0bis:3801674"
/db_xxef="c0bis:3801674"
/db_xxef="cbis:3801674"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/clone="IMAGE:293827"
/dev_stage="20 week-post conception fetus"
/dev_stage="20 week-post conception fetus
N98285 437 bp mRNA linear EST 10-APR-1996 za27h10.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:293827 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                    Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 437)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The Washu-Merck Est Project
Unpublished (1995)

Contact: Wilson RK
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop: 390.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                 N98285.1 GI:1269708
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Manualitis Eucharia; Frinaces; Catafinin; Hominidae; Homo.

M., Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Halliams, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Halliamson, A., Wohldmann, P. and Wilson, R.

The Washur, Exp Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 344
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl) gov) for further information.

Insert Length: 541 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N20300 472 bp mRNA linear EST 18-DEC-1995 yx43b10.s1 Soares melanocyte 2NbHM Homo saplens cDNA clone IMAGE:264475 3', mRNA sequence.
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/lab_host="ThiOB (ampicillin resistant)"
/note="Vector: p77130 (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Homin1dae; Homo.
181
                                                                                                                                                                                                                                     262 cagaaggetectggaaagagtgaatatgtgtegeatecagagagetgatggggattgtga 321
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                                                                                                                                                             ctcagaagccatacttcccattgcctccagctgttgcacggaggtttcacatcattttc
                                                                                                                                                                                 /clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 CCACAGGAAGAACACCATGGCAAGAGGAACAGTAACA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccacaggaagaaacaccatggcaagaggaacagtaaca
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/organism="Homo sapiens"
/db_xref="GDB:3874117"
/db_xref="taxon:9606"
/clone="IMAGE:264475"
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Location/Qualifiers
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N20300.1 GI:1125255
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N20300/c
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AUTHORS
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was deal be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=CMO-BT0687-210
300-297-f088513=2000-03-21£t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17

High quality sequence stop: 399.
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Organism="Homo sapiens"

/db_xref="taxon.9606"
/clone_lib="BT0687"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; Anin-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 // 716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 399)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
.M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                       EST 12-JUN-2000 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                      241 TGCTGGAATTACCAGCGTGAG-CACCATGCCGGGCTCACACGTTTGAGTTGATACCATTG 299
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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96.7%;
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Matches 385; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
Seq primer: -400P from Gibco.
                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p mRNA linear EST 27-JUL-2000 sapiens cDNA clone IMAGE:3183921 3',
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 362)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Oppublished (1997)
                                                                                                                                                                                                       1811
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Pred. No. 2.6e-44;
0; Mismatches 2; Indels
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hw25b05.x1 NCI_CGAP_Kid11 Homo
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BE463561
BE463561.1 GI:9509336
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Best Local Similarity 99.2%;
Matches 374; Conservative
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TITLE
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KEYWORDS
SOURCE
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Amodified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 13223/6-1323911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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AZ575795.1 GI:11562106
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1 (bases 1 to 345)
Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
Exon-trap tags from a 747D GenomeScreen(TM) Library
Unpublished (2000)
                                                                                                         /clone="IMAGE:3183921"
/clone_lib="NCI_GAAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tetecataggttaaaatgecaccaaaactggeetttgeetaatateettgaetatt 1750
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    362
    /organism="Homo sapiens"
/db_xref="taxon:9606"

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fatima Bonaldo.
81 c 6
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Gene Expression
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Matches 361; Conserv
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1. 510
/organism="Homo saplens"
/db_xref="taxon:9606"
/clon=lb="BN0114"
/dev_stage="Adult"
/dev_stage="Adult
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein.A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MR2-BN0114-020 S00-013-bl2&t3-2000-05-02&t4-1) Seq primer: puc 18 forward High quality sequence start: 21 High quality sequence start: 21 High quality sequence stop: 442.
                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 4.3e-34;
0; Mismatches 19
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                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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nes 304; Conservative
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Job time: 1753 sec
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                                                                                                                               Email: henkelg@aurorablo.com
Pools of cells were isolated from a GenomeScreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pamp'l and used to transform DHS-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .345
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cref="taxon:9606"
/clone_lib="deenetrap T47D Human Breast Carcinoma Library"
/tissue_type="Carcinoma"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 510)
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used
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/cell_type="Epithelial"
/cell_line="T470"
/note="Organ: Breast; Vector: pAmp-1; 3' RACE of
from genetrap pools; shotgun clone in pAmp-1 and
transform DH5-alpha competent bacteria."
77 82 q 73 t
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                               Corp.
ad, San Diego, CA 92121, USA
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APPLICANT: Puster, Lyn M
APPLICANT: Prustaci, Jana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 60/092,155
NUMBER OF SEQ ID NOS: 18
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                       agaagccaatagagagcaggagccacttta--tcaggtggcaggtgtcccgggcctccct
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Pred. No. 4.5e-76;
0; Mismatches 2;
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APPLICANT: Puster, Lyn M
APPLICANT: Fustaci, Jana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 7
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO
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                                                                                                                                                           Sequence 7, Application US/09146580A
Patent No. 6306653
GENERAL INFORMATION:
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COTHER INFORMATION: N
US-09-146-580-7
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US-09-146-580-11/c
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Best Local Simi
Matches 379;
                                                                                                            RESULT 2
US-09-146-580-7
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CUMPRIST STATE TO U.S.

ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
FILING DATE:
FLING DATE:
ACASSIFICATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELEPHONE: (248) 539-5050
INPORMATION FOR EQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TTELENDENESS: double
STRANDBURSS: double
STRANDBURSS: double
TO COMPATION TO THE COMPA
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OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
FEATURE:
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  /function= "(translation start:
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NAMEKEY:

LOCATION: 24090..25177

LOCATION: 24090..25177

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: 24110;

OTHER INFORMATION: 24110;

OTHER INFORMATION: Actidence= EXPERIMENTAL

OTHER INFORMATION: Actidence= EXPERIMENTAL

OTHER INFORMATION: Anumber= 2

FEATURE:

NAMEKEY: exon

LOCATION: 25524..26009

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: Actidence= EXPERIMENTAL

OTHER INFORMATION: Actidence= EXPERIMENTAL

OTHER INFORMATION: Actidence= EXPERIMENTAL

OTHER INFORMATION: Anumber= 3

OTHER INFORMATION: Anumber= 3
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OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
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/gene= "ACHE"
/number= 4
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LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OCHER INFORMATION: /evidence= EXPER:
OTHER INFORMATION: /genc="ACHE"
OTHER INFORMATION: /number= 4
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IDENTIFICATION METHOD: experimental
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
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LOCATION: 22465..22537
Farmington Hills
Michigan
                                                                     U.S.
                                                                     COUNTRY:
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                  GENERAL INFORMATION:
APPLICANT: Papsidero, Lawrence D
APPLICANT: Papsidero, Lawrence D
APPLICANT: Pustacat, Lyn M
APPLICANT: Futacact, Jana M
TILLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: 05/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER APPLICATION NUMBER: 60/092,155
BARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTL VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.0%; Score 302; DB 4; Length 311; Best Local Similarity 99.3%; Pred. No. 6.5e-59; Matches 302; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: N at position 162 is either A, C, G, or US-09-146-580-11
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STREET: 30500 No. 6025183thwestern Highway, Suite 410
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: N at position 101 is either A,
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Sequence 7, Application US/08814095
Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Sored, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (101)
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LOCATION: (162)
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LENGTH: 311
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complement (34528..34895)
WATION: /function= "arsenite resistance
                                                                                                                                                               NAME/KEY: exon
LOCATION: 28008..28129
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence- EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
FEATURE:
LOCATION: 28129..28131
FEATURE:
/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: exon
LOCATION: complement (32959..33094)
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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WATION: /gene= "AR"
WATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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/number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene"
                                                                                                                        27385..27387
                                                                                                   terminator
      OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                           ... LUCATION: COMPLEMENT (29664..29856); OTHER INFORMATION: /gene= "ARS"; OTHER INFORMATION: /number= 16
NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FEATURE:
                                                                                       NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
FEATURE:
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LOCATION: complement (30187..30274)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number=14
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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LOCATION: comp
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LOCATION: comp
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NAME/KEY: CDS
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US-09-167-681-45
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LENGTH: 8447
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APPLICANT: Liu, Xuessong
TITLE OF INVENTION: DAA FRAGMENTATION FACTOR INVOLVED IN
TITLE OF INVENTION: APOPTOSIS
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,702
FILING DATE: Concurrently Herewith
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Pred. No. 6.1e-40;
0; Mismatches 328;
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ATTORNEY/AGENT INFORMATION:
NAME: MCMILlian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512,418-3000
TELEPHONE: (512)474-757
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09061702
Patent No. 6165737
GENERAL INFORMATION:
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58.0%;
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Best Local Similarity 58.0
Matches 462; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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STRANDEDNESS: single
TOPOLOGY: linear
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US-09-061-702-1
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1660 TGTGAGTACCTGGTCATACGGGTCAGGGATAAGAATTGTCTCTGGGCTGAGGAATTC 1719
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APPLICANT: Wood, Thomas C.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Diane M.
TTILE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASTSEQ for Windows Version 3.0
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Patent INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard
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                                                                                               Length
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Pred. No. 7e-39;
0; Mismatches 83;
                                                                                            DB 4;
                                                                                                                                        51;
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APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                            Score 216.4; DB Pred. No. 1e-39;
                                                                                                                                        0; Mismatches
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83.2%;
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Best Local Similarity 76.9%;
Matches 286; Conservative
  - A,T,C
                                                                                                                                        258; Conservative
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US-09-078-294-9
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; OTHER INFORMATION: n
US-09-385-982-354
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                                                                                                                     Similarity
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US-09-078-294-9
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Best Local S
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GENERAL INCORMATION:
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS:
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: 09/328,111
EARLIER PILLING DATE: 1999-06-08
EARLIER PILLING DATE: 1999-06-08
EARLIER PILLING DATE: 1999-01-27
EARLIER PILLING DATE: 1999-01-27
EARLIER PILLING DATE: 1999-01-27
EARLIER PILLING DATE: 1999-01-27
SARILER FILLING DATE: 1999-01-27
SARILER FILLING DATE: 1999-01-27
SARILER FILLING DATE: 1999-01-27
SOTTWARE: FESSEQ FOR WINDOWS VERSION 3.0
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                                                                                                                                                                                                                                                                                                                               Score 217; DB 4;
Pred. No. 1.5e-39;
0; Mismatches 85
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Patent No. 6262334
                                                                                                                                                                                                                                                                                                                               Query Match 10.8%;
Best Local Similarity 76.4%;
Matches 279; Conservative
                                         LOCATION: (4827)...(4925)
NAME/KEY: CDS
LOCATION: (6322)...(6447)
NAME/KEY: CDS
LOCATION: (6543)...(6638)
NAME/KEY: CDS
LOCATION: (7137)...(7316)
NAME/KEY: CDS
                        (4827)...(4925)
CDS
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LOCATION: (1)...(631)
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LENGTH: 631
  LOCATION:
NAME/KEY:
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APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                      42060 CICCTGACCTCAAGTGATCTGCCTCGCCTCCCAAAGTGCTGGGATTACAGGCGTG 42001
42179 ATTCTCCTGCCTCAGCCTCCTGAATAGCTGGGATTACAGGCACCCA-ACACCACGCCCAG 42121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application PC/TUS9306251
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILINO DATE:

ATORNEY/AGRAT INFORMATION:

NAME:

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8586

TELECHONE: 516.742-443

TELEPHONE: 516.742-436

TELEFAX: 516.742-436

TELEFAX: 516.742-436

TELEFAX: 1230 901 SANS UR

INFORMATION FOR SEQ. ID NO: 80: SEQUENCE CHARACTERISTICS:

LENGTH: 841 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
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; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4 uv ...
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PCT-US93-06251-80/c
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                                  ttttagtagagacggggtttcccacgttggccgggctggtctcaaactcttgacctcaa 1396
                                                                                                                                                                    gtgaaccacccgcctgtgcctcccaaagtgctggaattaccagogtgagccaccatgccg 1456
                                                                                                                                                                                                                               1337 gigatecgeetgeeteageeteceaaagigetgggattacaggigtgageeaceatgeee 1396
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                                                                                                 1279 ttttagtagagatggggtttcaccatgttggtcaggctggtgtcaaactcctgacct--t 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Chang-En
APPLICANT: Wolling, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Best Local Similarity 81.4%; Pred. No. 2.5e-38;
Matches 258; Conservative 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACLASSITATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39 3317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (266) 622-4900
TELEPHONE: (266) 622-4900
TELEPHONE: (266) 63-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           1457 ggctcacacgtt 1468
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STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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1293 gatattacaggcgcccagccaccaccaccccgctgatttttgtattttagtagacggg 1352
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                                                                  560 crircaccarciregreaegeregereregarcicereaecreaegrearcearerecere 501
679 CACTGCAACCTCTGTCTCCTGGGTTCAAACGATTCTCCTGCCTCAGCCTCCCAAATAGCT 620
                                                                                                                                                                                                                                                    NAME/KEY: Pl-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126
TELEPHONE: (212) 756-4800
TELEFNAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/367,841A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morgan & Finnegan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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Sequence 81, Application PC/TUS9306251

Sequence 81, Application PC/TUS9306251

GENERAL INFORMATION:
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
COUNTRY: USA

COUNTRY: USA

STATE: USA
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             1293 gatattacaggcgcccagccaccacccccgctgatttttgtattttagtagagacggg 1352
                                                                                                  1353 gitticccacgitggccgggctggtctcaaactcitgaccicaagigaaccacccgccig 1412
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                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 212.2; DB 5;
Pred. No. 9.6e-39;
0; Mismatches 103;
                                                                                                                                                                                                                                                                          1473 ttgataccattgtgccattcctctttgg 1501
                                                                                                                                                                                                                                                                                                                   440 TAAATCTACTTCCCCTAGTGCTCATGTGG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEFRAN: 516-742-4343
TELEFRAN: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 81:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.5%;
Best Local Similarity 73.3%;
Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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; MOLECULE TYPE:
PCT-US93-06251-81
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1151 tttgttgttgtttggttgtttttttttttgagacagagtctcactctgttgcccaggctgga 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1211 gtgcagtggcacaatctcggctcattgcaacctccgcctccgcgttcaagtgattctct 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9740 CCTCAGGTGATCTACCCGCCTCGGCCTCTCAAAGTGCTGGGATTACAGGTTTGAGCCACT 9799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full length genomic sequence for PEDF plus flanking sequences
                                                                                                                                                                                                                                                                                                                                                                                            Length 22481;
                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Munroe, David J.
APPLICANT: HOUSMAN, DAVID E.
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 212.2; DB 5
82.5%; Pred. No. 2.4e-38;
iive 0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America ZIP: 02210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,629
FILING DATE: 07-0CT-1993
CLASSIFICATION: 435
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US-08-133-629-8/c
; Sequence 8, Application US/08133629
; Patent No. 5597694
                                                                                     22481 Base Pairs
                                                                                                                                                  TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
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                 TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full
OTHER INFORMATION: seq.
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 82.5
Matches 255; Conservative
                                                                                                                                Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
                                                                                                       TYPE: Nucleic Acid
STRANDEDNESS: Doub
                                                                                                                                                                                                                 NAME/KEY: P1-147
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  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                               FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     octcaagtgaaccacccgcctgtgcctcccaaagtgctggaattaccagcgtgagccacc 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9740 ccrcaggrgarcracccgccrcagccrcrcaaagrgcrgggarracaggrrrgagccacr 9799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-07201-43

Sequence 43, Application PC/TUS9507201

GENERAL INFORMATION:

APPLICANT: Chader, Gerald J.; Becerra, Sofia

APPLICANT: Taniwak, Takayuki

TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC

TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: New York

STATE: New York
                                                                                                         1;
                                                            Length 22481;
                                                                                                         Indels
                                                              Score 212.2; DB 4;
Pred. No. 2.4e-38;
                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMUTEY: New FOLK
COMPUTEY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION NUMBER: 08/367,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION NUMBER: 08/257,963
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: 24-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20264126PCT
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REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                            10.5%;
82.5%;
                                                                                   Best_Local Similarity 82.5
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1451 atgccgggc 1459
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US-08-367-841A-43
                                                            Query Match
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FILING DATE: 18-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-07-906-871-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                   1298 tacaggcgcccagccaccaccccgctgatttttgtattttagtagagacggggtttt 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 282;
                                                                                                                                                                                                                                                                                                                    Indels
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Sequence 15, Application US/07906871

Patent No. 5340739

GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Avraham, Shalom
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMEN;
TITLE OF INVENTION: THEREOF

UNDRESS OF SEQUENCES: 18

CORRESPONDENCE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 cccaaagtgctggaattaccagcgtgagccaccatgccgggc 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 CCCAAAGTGCTGGGATTACAGGTGTGAGGCCACCACGCCCAGC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20036

ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               Score 211.6; DB 1;
Pred. No. 9.6e-39;
6; Mismatches 35;
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FILING DATE: 19920103
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
                                 M0828/7001
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                36,816
                                                                              TELERA: 617-720-2441
TELEX: 92-1742 EZEKIEL
INPORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
              REGISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: M
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                               Query Match 10.5%;
Best Local Similarity 85.1%;
Matches 240; Conservative
Greer, Helen
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STATE: DC
COUNTRY: USA
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US-08-133-629-8
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PRICA TOWN JAYS.

PRICATION NUMBER: PCT/US89/03051
FILING DATE: 13-UUL-1889
PRICATION NUMBER: PCT/US89/03051
PRICATION NUMBER: US/O7/224,035
FILING DATE: 13-UUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELA A
REGISTRATION NUMBER: 33,851
REFERNENCE/OCKET NUMBER: 0627.283000
TELEPHONE: (202)833-753
TELEPHONE: (202)833-8716
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17327 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: DATA
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9597..9744
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TITLE
                                                                   October 7, 2002, 09:01:55; Search time 2534.54 Seconds (without alignments) 16653.446 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

% Query Score Match Length DB ID

> No No

SUMMARIES

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AC010465 Homo sapi AC025457 Homo sapi AC025132 Homo sapi AR174328 Sequence AF266504 Homo sapi AF110384 Homo sapi AF220210 Homo sapi AF220210 Homo sapi	Sequenc Sequenc Sequenc Homo sa Homo sa Homo sa	Humar Homo Homo Homo Homo Homo Homo	ນ໙໙໙໙຺໙໙໙຺໙໙	: = = = = = = = = = = = = = = = = = = =
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5.1 107819 5.1 140734 5.1 143372 1.3 3117 4.6 1349 9.0 384	7.9 472 7.9 472 5.0 311 2.1 61101 2.1 146376 2.0 22426	2.0 53402 2.0 112219 1.9 146443 1.9 149899 1.9 190069 1.9 174231 1.9 213464	9 123464 135044 8 135044 8 149425 8 191754 8 86428 8 153937 8 153937 8 135016 8 133273	1.8 168394 1.8 168729 1.8 178601 1.8 178601 1.8 88698 1.8 18698 1.8 180964 1.8 180964 1.8 180964
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ALIGNMENTS

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                                               Direct Submission
Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13470140.
Draft Sequence Produced by DOE Joint Genome Institute
 Submitted (28-MAR-2001) DOB Joint Genome Institute, 2800 Mitchell Live, Walbut Creek, CA 94598, USA 4 (bases 1 to 107819)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
Www.shgc.stanford.doc.gov
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.4.
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Pred. No. 3e-292;
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22135 c 21940 g 31767
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/db_xref="taxon:9606"
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Submitted (28-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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HOMO sapiens chromosome 5 clone CTD-2202K16, complete sequence.
AC025457
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DUE Joint Genome Institute and Stanford Human Genome Center. Unpublished
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Jose Sandard (09-MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459

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Doe Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

L Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Jun 8, 2001 this sequence version replaced gi:13470150.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >-40 99.5% of Sequence;

Estimated Total Number of Errors is 0.3.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata; Catarrhini; Hominidae: Homo.

Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.

E 1 (bases 1 to 143372)

L Unpublished

L Unpublished

E 2 (bases 1 to 143372)

S DOE Joint Genome Institute.

S DOE Joint Genome Institute.

D Incert Submission

L Submitted (26-ANA-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2011 this sequence version replaced gi:7711706.
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HOMO sapiens chromosome 5 clone CTD-2201J22, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
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Consensus quality: 131953 bases at least Q40
Consensus quality: 136047 bases at least Q30
Consensus quality: 13762 bases at least Q30
Consensus quality: 13752 bases at least Q30
Estimated insert size: 119000; pulse field gel estimation
Estimated insert size: 10572; sum-of-contigs estimation
Quality coverage: 7.17 in Q20 bases; pulse field gel estimation
Quality coverage: 5.98 in Q20 bases; pulse field gel estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
Web site: http://www.jgi.doe.gov
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 768)

Pan, J., Kunkel, E.J., Gosslar, U., Lazarus, N., Langdon, P.,

Broadwell, K., Vierra, M. A., Genovess, M.C., Butcher, E.C. and Soler, D.

Cutting edge: A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial cells in mucosal tissues
J. Immunol. 165 (6), 2943-2949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA linear PRI 27-SEP-2000 epithelial chemokine mRNA, complete
2628 GCTGGYINNTCCCAAGCGGTGGTGTTGCCARGANKTNTTGGARGTGATAATGGGANANAC
                                                                                                                                                                               --agaggcactgagtctccataggttaaaatgccaccaaaactggccttt-gcctaatat
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                                                                                                                                             gctggctagtcccaagcggtggtgttgccaggatgtcttggaggtgatatagggacacac
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Gosslar, U., Pan, J., Kunkel, E.J. and Butcher, E.C.
Direct Submission
Submitted (10-MAY-2000) Department of Pathology, Stanfo
University, 3801 Miranda Ave, Palo Alto, CA 94304, USA
Location/Qualifiers
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MEDLINE
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                                                                                                                                                                                     Length 3117;
                                                                                                                                                     others
                  linear
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Papsidero, L.D., Dyster, L.M. and Frustaci, J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 6 23-OCT-2001;
Location/Qualifiers
1.3117
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9
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Pred. No. 3.7e-228;
73; Mismatches 92;
                   DNA
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                3117 bp
from patent US 6306653.
                                                                                                                                          /organism="unknown"
582 c 566 g
                                           GI:17914648
                                                                                                                                                                                     51.3%;
86.5%;
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2; Conservative
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Unclassified.
                 AR174328
Sequence 6 f
AR174328
AR174328.1
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Best Local Simi
Matches 1172;
RESULT 4
AR174328
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/product="CCKI protein"
/protein_id="AAG43193.1"
/db_xref="CI:12002127"
/tanslation="MQORGLAIVALAVCAALHASEAILPIASSCCTEVSHHISRRLLE
RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear PRI 23-JUL-2000 (SCYA28) mRNA, complete cds.
     Zhang, W., He, L., Yuan, Z., Wan, T. and Cao, X.
Direct Submission
Submitted (01-DEC-1998) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Blotechnolog Institute,
800 Xiangyin Roâd, Shanghai 200433, P.R.China
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100.0%; Pred. No. 2.9e-104;
iive 0; Mismatches 0;
                                                                              /organism="Homo saplens"
/db_xref="taxon:9606"
1. 1349
                                                                                                                                                      /note="similar to TECK"
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                                                             Location/Qualifiers
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AF220210
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                                                                                                                  /gene="CCK1"
55. .438
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Matches 497
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KEYWORDS
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ORIGIN
     AUTHORS
TITLE
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RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
191 c 163 g 171 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1349)
Zhang,W., He,L., Yuan,Z., Wan,T. and Cao,X.
A novel CC chemokine homology with TECK
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Homo sapiens CCK1 protein (CCK1) mRNA, complete cds.
AF110384
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ilarity 100.0%; Pred. No. 2.8e-104;
Conservative 0; Mismatches 0;
                                                            /codon_start=1
/product="mucosae-associated
/protein_id="AAG16691.1"
/db_xref="G1:10312152"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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53. .436
                                                 /note="chemokine; MEC"
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TGGCCATGATTGGTTGT 497
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TITLE
JOURNAL
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Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Papsidero, L.D., Dyster, L.M. and Frustaci, J.M. Detection and treatment of breast disease Patent: US 6306653.A 7 23-ocr-2001;
Location/Qualifiers
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Pred. No. 4e-77;
0; Mismatches
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Sequence 175 from Patent WO0194629.
AX329666
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/db_xref="taxon:9606"
                                                                                                                                                   /organism="unknown"
91 c 97 g
             GI:17914649
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Best Local Similarity 99.5%;
Matches 379; Conservative
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RVMORIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHGKRNSNRAHQGKHETYGHKTPY"
91 c 99 g 81 t
                                                                                                                                                  Soto, H., Vicari, A. and Zlotnik, A.

Soto, H., Vicari, A. and Zlotnik, A.

Direct Submission

Birect Submission

California Ave, Palo Alto, CA 94304, USA

Location/Qualifiers
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 384)
Wang, W., Soto, H., Oldham, E.R., Buchanan, M.E., Homey, B., Catron, D., Jenkins, N., Copeland, N.G., Gilbert, D.J., Nguyen, N., Abrams, J., Kershenovich, D., Smith, K., McClanahan, T., Vicari, A.P. and
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100.0%; Pred. No. 2.8e-78;
tive 0; Mismatches 0;
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/gene="SCYA28"
/codon_start="
/product="CC chemokine CCL28"
/protein_id="AAR87205.1"
/db_xref="GI:9392591"
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Sequence 7 from patent US 6306653.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.0
Matches 384; Conservative
              Homo sapiens
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          agcatttaatttatttattttcctgacatttctgcaagctttgtatatttccactt
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Papsidero,L.D., Dyster,L.M. and Frustaci,J.M.
Detection and treatment of breast disease
Patent: US 6306653.A 11 23-0CT-2001;
Location/Qualifiers
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Pred. No. 2.1e-59;
0; Mismatches 2;
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Sequence 11 from patent US 6306653.
AR174333
AR174333.1 GI:17914653
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Best Local Similarity 99.3%;
Matches 302; Conservative (
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Cancer gene determination and therapeutic screening using signature
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Pred. No. 3.7e-73;
0; Mismatches 2;
                                   Score 361.8; DB 6;
Pred. No. 3.7e-73;
0; Mismatches 2;
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Avalon Pharmaceuticals (US)
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Shirten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhaglater, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M. Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Ilaev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonall, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Marquis, N., McMens, L., Mihova, T., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, L., Pieterson, K., Pieterson, K., Pieters, R., Marquis, J., Norman, C. H., O'Connor, T., Pieterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Lirell, A., Travers, M., Triglilo, J., Yossillev, H., Viel, R., Vo, A., Lesearch, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                           ACO83975 61101 bp DNA linear HTG 08-OCT-2000 Homo sapiens chromosome 8 clone RP11-391E1 map 8, LOW-PASS SEQUENCE
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                      AC083975.1 GI:10
HTG; HTGS_PHASE0
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                                                                                                                                                                                              Homo sapiens
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KEYWORDS
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ap of 100 bp candidate of 702 bp in length ap of 100 bp canting of 714 bp in length ap of 100 bp in length conting of 700 bp in length
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f 702 bp in length
100 bp
f 703 bp in length
                            34633; gap of 100 bp 35334; contig of 701 bp in length 35434; gap of 100 bp in length 36127; contig of 693 bp in length
                                                                                                                                             100 bp
of 694 bp in length
                                                                                                                                                                                                        21: gap of 100 bp
37752: contig of 731 bp in length
52: gap of 100 bp
38574: contig of 722 bp in length
74: gap of 100 bp
39389: contig of 715 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (21: gap of 100 bp 41013: contig of 692 bp in length 13: gap of 100 bp 11811: contig of 698 bp in length
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48200: contig of 713 bp in length
00: gap of 100 bp
49010: contig of 710 bp in length
10: gap of 100 bp
49815: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 711 bp in length
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54731: gap of 100 bp
55412: contig of 681 bp in length
55512: gap of 100 bp
56246: contig of 734 bp in length
   in length
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of 732 bp
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50619: contig of 704 bp
19: gap of 100 bp
51404: contig of 685 bp
of 701 bp
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47387: contig of 1
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45782: contig c
45882: gap of
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36921: contig
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48200: contig
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54631: cont<sup>4</sup>
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41013: cont
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42606: cont
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53820: con
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Query Match 12.1%; Score 243.6; DB 2; Length 61101; Best Local Similarity 53.6%; Pred. No. 8.2e-46; Matches 444; Conservative 0; Mismatches 373; Indels 12; Gaps 3;

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Qy 851 ttatittgtcatttagagttcataaatattagggtttattttctaaatagaatagtttaa 910

53953 CTCTACCTGTTTGGNGGAAAACCCTGCGCAAATCANACAAGTTATGTGTTTCCATAATA 54012 54364 TCTCAGGTAATCCACCCACTTTGGCCTCCCAAAGTGCTGGGATAACGAGCCCGAGCCACC 54423 54013 TAATGGTGGGACAGGCA-----TAGGCTAGACATTCCCCTTGCAAAAGGGGGAAATG 54064 ctgatactgaaaagaacaaaaagcctgccttctgcccagaaccttttgcctccccagt 1030 cagttettggageageactagttaggggeecegagtteggeettetgtgtggtgatttta 1090 1211 gigcagiggcacaatcicggcicatigcaacciccgccicccgcgticaagigaticici 1270 1091 cgctctgcctaaacaaggagcctacatcttttagctcctattccacccttctcacacgtt 1150 cctcaagtgaaccaccgcctgtgcctcccaaagtgctggaattaccagcgtgagccacc 1450 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTTTTGGNNNGCCTCACT - - - TTTTNNTATT 54065 GGGGAAATAAGAAAGAAAGAGGGTACCTGGACTTCCAAATCAAAATTCTAGCAAGGCA 1271 tgcctcagcctcccaagtaactgatattacaggcgcccagccaccacccgctgattt actaaatataacttcaaaacgtctagtttgagtagctaccgttgtttggattgaaatttt 54304 TTGTATTTTAGTAAAGACAGGGTTTCATCATGTTGGCCAGGCTGGTCTTGAACTCTTGA ttgtatttttagtagagacgggttttcccacgttggccgggctggtctcaaactcttga 53896 1391 54185 1331 ò qq g g q qq g g ò ŏ ò ò ò ò ò ò ò

DUGANISM

Homo sapiens

BUKATYOTS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

BUKATYOTS, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

MARMMALIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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I (bases 1 to 14637, Balley,M., Barbaria,J., Blankenburg,K.,

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AUTHORS TITLE JOURNAL

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12980, 13357
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11362. .11452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCING READ COVERACE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                Submitted (08-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 146376)
                                                                                                                                                                                                                                                                                                                                                         Submitted (08-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 146376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 146376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 14, 2001 this sequence version replaced gi:13489132. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weenstock, G., Wainstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Naylor, S.L., Nelson, D. and Gibbs, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANNOTATION OF FEATURES:
                                                                                                                               (bases 1 to 146376)
                                                                                                                                                     Worley, K.C.
Direct Submission
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Direct Submission
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repeat_region

repeat_region

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Location/Qualifiers

QUALSTAT-REPORT

FEATURES

.146376

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repeat_region

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Direct Submission
Submitted (10-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MPO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
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/db_xref="taxon:9606"
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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complement(21253. 21311)
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                  complement(17700. .17843)
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AL359540 149916 bp DNA linear HTG 08-FEB-2002 Homo sapiens chromosome 1 clone RP4-534D1 map p34.1-35.3, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       10834 CTGCCTCAGCCTCCAGAGTAGCTGGAACTACAGATGTGC-GCCACCATGCCCGGCTAATT 10776
                                                                                                                                                                                                                                 10775 TTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTG 10716
10954 ATTATGTTATATTATATATTTTTTTTGAGACAGGGTCTCACTCTATTGCCCAGGCTGG 10895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Bly Dye; 100% of reads
Consensus quality: 149780 bases at least Q40
Consensus quality: 149824 bases at least Q30
Consensus quality: 149855 bases at least Q20
Insert size: 149916; sum-of-contygs
Insert size: 150837; 6.6% error; agarose-fp
Quality coverage: 9.27x in Q20 bases; sum-of-contigs Quality
coverage: 9.22x in Q20 bases; agarose-fp
                                                                                                                ttgcctcagcctcccaagtaactgatattacaggcgcccagccaccacaccccgctgatt
                                                                                                                                                                                             tttgtatttttagtagagacggggttttcccacgttggccgggctggtctcaaactcttg
                                                                        10894 AGIGCAGIAGCAIGAICIIGGCICACIGCAACCICIGCCICCCAGGIICAAGCGAIICIC
                                        agigoagigoacaaicicggoicaitgoaacciccgcciccgcgitcaagigaitcic
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Location/Qualifiers
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Submitted (28-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 107819)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 8, 2001 this sequence version replaced gi:13470140.
Praft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.5% of
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/db_xref="taxon:9606"
/chromosome="5"
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DOE Joint Genome Institute.
DoE Joint Genome Institute.
Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 140734)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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AC025457
HGC025457.5 GI:14329097
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Drive, Walnut Greek, CA 94598, USA
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                     Genome Institute
Drive, Walnut Creek, CA 94598, USA on Jun 8, 2001 this sequence version replaced gi:13. Traft Sequence Produced by DOE Joint Genome Institut www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.5% of Seq
Estimated Total Number of Errors is 0.3.
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:7711706.
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                                                   ggtaagagcccagtagtgttcataagaagccaatagagagcaggagccactttatcaggt
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Consensus quality: 131953 bases at least Q40
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Homo sapiens chromosome 5 clone
SEQUENCE, 9 unordered pieces.
AC022132
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Sequencing of Human Chromosome
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Mammalia; Eutheria; Primates;
1 (bases 1 to 143372)
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Center Project Name: 704971
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DOE Joint Genome Institute.
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AC022132.5 GI:13699628
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Consensus quality: 137362 bases at least Q20
Estimated insert size: 119000; pulse field gel estimation
Estimated insert size: 142572; sum-of-contigs estimation
Quality coverage: 7.17 in Q20 bases; pulse field gel estimation
Quality coverage: 5.98 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1056
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                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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t 802 others
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ilarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches

    .143372
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Best Local Similarity
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mRNA linear PRI 27-SEP-2000 epithelial chemokine mRNA, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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tottttagotoctattocaccottotoacacgtttttgttgttgtttggttggttgtttttt 1176
                                                                                                        ggcaggtgtcccgggcctcctgctggctagtcccaagcggtggtgttgccaggatgtct
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                                   tgagacagagtctcactctgttgcccaggctggagtgcagtggcacaatctcggctcatt
                                             AF266504 768 bp
Homo sapiens mucosae-associated
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AF266504.1
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PRI 02-JAN-2001

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/translation="MOORGLAIVALAVCAALHASEAILPIASSCCTEVSHHISRRLLE
RVNMCRIQRADGDCDLAAVILHVKRRRICVSPHNHTVKQWMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
                                                                                                                                                                                               Unpublished

2 (bases 1 to 1349)

Zhang,W., He,L., Yuan,Z., Wan,T. and Cao,X.

Direct Submission

Submitted (01-DEC-1998) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnolog Institute,

800 Xiangyin Road, Shanghai 200433, P.R.China
                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1349)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1349;
                    1349 bp mRNA linear
Homo sapiens CCK1 protein (CCK1) mRNA, complete cds.
AF110384
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                                                                                                                                                                      Zhang, W., He, L., Yuan, Z., Wan, T. and Cao, X.
A novel CC chemokine homology with TECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.6%; Score 497; DB 9; Le
100.0%; Pred. No. 3.2e-261;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 1349
Acranism="Homo sapiens"
Ab_xref="taxon:9606"
1. 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG43193.1"
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                                        DEFINITION
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REFERENCE
AUTHORS
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TITLE
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    1 (bases 1 to 768)
Pan, J., Kunkel, E.J., Gosslar, U., Lazarus, N., Langdon, P.,
Broadwell, K., Vierra, M.A., Genovese, M.C., Butcher, B.C. and Soler, D.
Cutting edge: A novel chemokine ligand for CCR10 and CCR3 expressed
J. Immunol. 165 (6), 2943-2949 (2000)
10975800
                                                                                                                                                                                                                                                                                                                             /protein_id="AaG16691.1"
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KHHGKRNSNRAHQGKHETYGHKTPY"
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/product="mucosae-associated epithelial chemokine"
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                                                                                                                         2 (bases 1 to 768)
Gosslar,U., Pan,J., Kunkel,E.J. and Butcher,E.C.
Direct Submission
Submitted (UnAY-2000) Department of Pathology, Stanford
University, 3801 Miranda Ave, Palo Alto, CA 94304, USA
Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 768;
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100.0%; Pred. No. 3.2e-261;
ive 0; Mismatches 0;
                                                                                                                                                                                                            1. 768
/organism="Homo sapiens"
/organism="Homo sapiens"
/ob_xref="taxon:9606"
/chromosome="5"
53. .436
                                                                                                                                                                                                                                                                                     /note="chemokine; MEC"
Mammalia; Eutheria; Primates;
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                                        697 ctcaaactcctgggctcaagcgatcctcccaccttagcctcccaaagtactgggattata 756
241 GTTAAGCAGTGGATGAAAGTGCAAGCTGCCAAGAAAAATGGTAAAGGAAATGTTTGCCAC
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Papsideroi.Lo., Dyster.L.M. and Frustaci,J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 6 23-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.5%; Score 313; DB 6; Lø
Best Local Similarity 100.0%; Pred. No. 3.3e-160;
Matches 313; Conservative 0; Mismatches 0;
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6 from patent US 6306653.
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1. .3117
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582 c 566 q
                                                                                                 506 tacggccataaaactccttattag 529
                                                                                                                361 TACGGCCATAAAACTCCTTATTAG 384
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Sequence 6 from patent U
AR174328
AR174328.1 GI:17914648
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/codon_start=1
/product_="CC chemokine CCL28"
/product_="CC chemokine CCL28"
/db_xref="G1:9392591"
/db_xref="G1:9392591"
/xranslation="MQRGAIVALAVCAALHASEAILPIASSCCTEVSHHISRRLLE
//WCRIORAGGDCDLAAVILHVKRRRICVSPHNHTVKQMMKVQAAKKNGKGNVCHRK
KHHGKRNSNRAHQGKHETYGHKTPY"
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HOMO sapiens CC chemokine CCL28 (SCYA28) mRNA, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNAX Research Institute,
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J. Biol. Chem. 275 (29), 22313-22323 (2000)
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512 cataaaactccttattagagagtctacagataaaatctacagagacaattcctcaagtgga
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Best Local Similarity 100.0%; Pred. No. 3.5e-199;
Matches 384; Conservative 0; Mismatches 0;
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2 (bases 1 to 384)
Soto, H., Vicari, A. and Zlotnik, A.
Direct Submission
Submitted (Jo-DEC-1999) Immunobiology, DN
California Ave, Palo Alto, CA 94304, USA
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Yound, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1813 atagatgaggaaatttgaggctcttagaggtaaaatgacttgcccaggtcacacaggaag 1872
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Patent: WO 0194629-A 5359 13-DEC-2001
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/db_xref="taxon:9606"
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Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Papsidero,L.D., Dyster,L.M. and Frustaci,J.M. Detection and treatment of breast disease Patent: US 6306653-A 7 23-OCT-2001; Location/Qualifiers 1.381
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Best Local Similarity 100.0%; Pred. No. 8e-128;
Matches 254; Conservative 0; Mismatches 0;
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Pred. No. 1.5e-141;
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Sequence 175 from Patent WO0194629.
AX329666.1 GI:18102644
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/db_xref="taxon:9606"
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                                     FEATURES
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Gaps

FEATURES

SOURCE

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Consensus quality: 117979 bases at least Q40
Consensus quality: 124608 bases at least Q30
Consensus quality: 12692b bases at least Q30
Consensus quality: 12692b bases at least Q30
Consensus quality: 12692b bases at least Q30
Estimated insert size: 142240; agarose-fp estimation
Quality coverage: 6.99 in Q20 bases; agarose-fp estimation
Quality coverage: 7.75 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is belleved to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be preserved.
* the accession number will be preserved.
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 11718 34238: contig of 11717 bp in length
* 48385 48384: gap of unknown length
* 48385 880643: contig of 13259 bp in length
* 86744 88722: contig of 13259 bp in length
* 88723 gapt of unknown length
                                                                                                                                                                                      129427 bp DNA linear HTG 23-APR-2001 Homen sapiens chromosome 19 clone CTD-2223D2, WORKING DRAFT SEQUENCE, 11 ordered pieces.
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Catarrhini; Hominidae; Homo.
                  745 actgggattataggtgtgagccacagtgcctggcctaattattttcttgtgatcaaattc 804
                                     bp in length
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of 9601 bp in length
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AC020929.4 GI:13752692
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Center clone name: CITB-H1_2223D2
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Unpublished
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Direct Submission
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91861:
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                  PAT 17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgctgtcatccttcatgtcaagcgcagaagaatctgtgtcagcccgcacaaccatactgt 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaagaaacaccatggcaagaggaacagtaacaggcacatcaggggaaacacgaaacata 507
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                  linear
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Papsidero,L.D., Dyster,L.M. and Frustact,J.M.
Detection and treatment of breast disease
Patent: US 6306653-A 11 23-0CT-2001;
Location/Qualifiers
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Upases 1 to 104)

Papsidero, L. D., Dyster, L.M. and Frustaci, J.M.

Detection and treatment of breast disease

Patent: US 6306633-A 8 23-0CT-2001;

Location/Qualifiers
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Pred. No. 2.8e-99;
0; Mismatches 2;
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Sequence 11 from patent US 6306653.
AR174333
AR174333.1 GI:17914653
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24 c 15 g
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99.3%;
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Best Local Similarity 100.
Matches 104; Conservative
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AUTHORS

RESULT

FEATURES

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukaladier, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McClurk, A., McKenan, K., Marquis, N., McEwan, P., McClurk, A., Marquis, N., McBwan, P., McClurk, A., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Wux, Wyman, D., Ye, W.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACO21625 164652 bp DNA linear HTG 28-MAR-2000 Homo sapiens clone RP11-384E6, WORKING DRAFT SEQUENCE, 34 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4%; Score 68; DB 2; Length 129427; 100.0%; Pred. No. 1.1e-25; tive 0; Mismatches 0; Indels 0
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                121814: Contig of 12185 bp in length 121914: gap of unknown length 124913: Contig of 3018 bp in length 125022: gap of unknown length are gap of 4395 bp in length.
                                                                                                                                                                                                                                                                                                                          /clone_lib="CalTech human BAC library D" a 34031 c 31504 g 31737 t 1000 others
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                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
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gap of
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AC021625.2 GI:7331453
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Matches 68; Conservative
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AC021625
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NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                             Center cloud name: 384_E_6

Sequencing vector: M13, M77815; 100% of reads
Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145159 bases at least Q40
Consensus quality: 155420 bases at least Q30
Consensus quality: 159351 bases at least Q20
Insert size: 161352; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
              Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5880
                                                                                                                                                                                                                                                                                                                                                                                                                         of 100 bp
contig of 1296 bp in length
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f 1540 bp in length
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f 1710 bp in length
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contig of 1732 bp in length
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contig of 2033 bp in length
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51: gap of 100 bp
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31228: contig of 4225 bp in length
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38469: contig of 3033 bp in length
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79365: contig of 4997 bp in length
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contig of 4500 bp in length
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contig of 4821 bp in
Web site: http://www-seg.wi.mit.edu
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51475: contig of 4288 bp
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83211: contig of 3746 bp
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in length

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83212 83311; gap of 100 bp 83312 88101; contig of 4790 bp in length 88102 88201; gap of 100 bp 88102 83785; contig of 5584 bp in length 93786; gap of 100 bp 93786 93885; gap of 100 bp 100508 1008158; contig of 5522 bp in length 100408 100507; gap of 100 bp 100508 108158; contig of 7651 bp in length 108159 10828; gap of 100 bp 115531; contig of 7373 bp in length 115632 115731; gap of 100 bp 115532 115731; gap of 100 bp 125489 12588; gap of 100 bp 125489 12588; gap of 100 bp 125489 135013; contig of 100 bp 136113; gap of 100 bp 149101; contig of 12997 bp in length 149111 149210; contig of 15442 bp in length.
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/clone_lib="RPCI-11 Human Male BAC"
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L Submitted (15-5700) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beljing, Beljing 100101, PR. Chinese Academy of Sciences, Datun Road, Beljing, Beljing 100101, PR. Chinese 1 to 172805)

Bao,J., Bao,Q., Bao,W., Blan,X., Cao,T., Chen,C., Chen,J., Ding,H., Bong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,W., Li,W., Li,W., Li,Y., Luo,C., Luo,J., Niu,Y., Gio,O., Gi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,X., Tao,R., Wang,X., Wang,X., Wang,J., Wang,J., Wang,L., Wang,R., Wang,X., Wang,X., Yu,B., Zang,Y., Zhang,X., Zhu,B., Zhu,B., Zhu,N.,
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Homo sapiens chromosome 3 clone RP11-785A7 map 3p, complete
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Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 172805)
Xiong, H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y.,
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Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
Chen, Z., and Huang, M.
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100.0%; Pred. No. 1.1e-25;
ive 0; Mismatches 0; Indels
                                  83312. 88101 /note="assembly_fragment"
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Best Local Similarity 100.
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VERSION
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